

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2003, 15:29:12 ; Search time 48 Seconds
(without alignments)
3845.813 Million cell updates/sec

Title: US-09-830-972-2
Perfect score: 5848
Sequence: 1 MEDIDQSSLVSSSTDSPRP.....VKDAMAKIQAKIPGLKRRKAD 1163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
- 7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
- 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
- 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
- 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
- 17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
- 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5848	100.0	1163	23	ABB81074	Rat neurotransmitt
2	5846	100.0	1163	21	AAAY71310	Rat neurite growth
3	5840	99.9	1162	21	AAAY71557	Rat Nogo A truncat
4	5823	99.6	1163	21	AAAY71384	Alternative versio
5	4921	84.1	974	21	AAAY71560	Rat Nogo A protein
6	4403.5	75.3	1192	22	AAU04591	Human Nogo protein
7	4403.5	75.3	1192	23	ABP68600	Human pancreatic c
8	4398.5	75.2	1192	21	AAAY56967	Human MAGI polypep
9	4398.5	75.2	1192	22	AAB82349	Human NOGO-A prote
10	4398.5	75.2	1192	23	ABB81078	Human neurotransmi
11	4398.5	75.2	1192	23	ABG30938	Human NogoA protei
12	4276.5	73.1	1178	21	AAAY71311	Human neurite grow
13	4116	70.4	1246	22	AAU33228	Novel human secret
14	4023	68.8	803	21	AAAY71562	Rat Nogo A protein
15	3714	63.5	737	21	AAAY71386	Rat Nogo A protein
16	3699.5	63.3	746	21	AAAY71391	Rat Nogo A protein
17	3651.5	62.4	736	21	AAAY71398	Rat Nogo A protein
18	3630.5	62.1	732	21	AAAY71399	Rat Nogo A protein
19	3494	59.7	695	21	AAAY71387	Rat Nogo A protein
20	3436	58.8	684	21	AAAY71394	Rat Nogo A protein
21	3385.5	57.9	983	24	ABU11573	Human MDDT polypep
22	3280.5	56.1	893	21	AAAY95012	Human secreted pro
23	2779	47.5	552	21	AAAY71388	Rat Nogo A protein
24	2500.5	42.8	642	19	AAW58383	Human secreted pro
25	2500.5	42.8	642	22	AAB90682	Human BG160_1 prot
26	2432	41.6	502	21	AAAY71396	Rat Nogo A protein
27	2388	40.8	475	21	AAAY71389	Rat Nogo A protein
28	2291	39.2	457	21	AAAY71392	Rat Nogo A protein
29	1987	34.0	403	21	AAAY71563	Rat Nogo A protein
30	1868	31.9	417	21	AAAY71393	Rat Nogo A protein
31	1801	30.8	356	21	AAAY71390	Rat Nogo A protein
32	1795.5	30.7	374	21	AAAY71397	Rat Nogo A protein
33	1416	24.2	361	21	AAAY71385	Alternative versio
34	1411.5	24.1	360	21	AAAY71383	Rat neurite growth
35	1411.5	24.1	360	23	ABB81076	Rat neurotransmitt
36	1405.5	24.0	359	21	AAAY71558	Rat Nogo A protein
37	1191	20.4	373	21	AAB24242	Human Nogo B prote
38	1191	20.4	373	21	AAAY56969	Human MAGI polypep
39	1191	20.4	373	21	AAAY53624	A bone marrow secr
40	1191	20.4	373	22	AAB82350	Human NOGO-B prote
41	1191	20.4	373	23	ABP68601	Human pancreatic c
42	1191	20.4	373	23	ABB81079	Human neurotransmi
43	1191	20.4	373	23	AAM47954	Human RTN4B SEQ ID
44	1183	20.2	373	23	ABG30937	Human NogoB protei
45	1063	18.2	284	21	AAAY95030	Human clone vb22_1

ALIGNMENTS

RESULT 1

ABB81074

ID ABB81074 standard; Protein; 1163 AA.

XX

AC ABB81074;

XX

DT 05-NOV-2002 (first entry)

XX

DE Rat neurotransmitter receptor protein Nogo-A.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; rat; receptor.

XX

OS Rattus norvegicus.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.

XX

PF 28-JUN-2001; 2001US-0893348.

XX

PR 19-MAY-1998; 98IL-0124500.

PR 21-JUL-1998; 98WO-US14715.

PR 22-DEC-1998; 98US-0218277.

PR 19-MAY-1999; 99US-0314161.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonogo A;
PI Moalem G;

XX

DR WPI; 2002-607255/65.

DR N-PSDB; ABN86600.

XX

PT Promoting nerve regeneration and preventing neuronal degeneration in
PT the central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides -

XX

PS Example 5; Page 44-47; 93pp; English.

XX

CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease

CC is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
 CC neuropathies associated with various diseases, including but not limited
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
 CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
 CC disease, or lipoproteinemia. The present sequence represents the rat
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific
 CC antigen.

XX

SQ Sequence 1163 AA;

Query Match 100.0%; Score 5848; DB 23; Length 1163;
 Best Local Similarity 100.0%; Pred. No. 1.1e-296;
 Matches 1163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60

Db 1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60

Qy 61 PAAGLSAAVPPAAAAPLLDFFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120

Db 61 PAAGLSAAVPPAAAAPLLDFFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120

Qy 121 PAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPSTPAAPKRRGSGSVDETLFALP 180

Db 121 PAAAVLPSKLPEDDEPPARPPPPAGASPLAEPAAPSTPAAPKRRGSGSVDETLFALP 180

Qy 181 AASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240

Db 181 AASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240

Qy 241 GNLSAVSSSEG TIETLNEASKELPERATNPFVNRDLAEFSELEYSEMSSFKGSPKGES 300

Db 241 GNLSAVSSSEG TIETLNEASKELPERATNPFVNRDLAEFSELEYSEMSSFKGSPKGES 300

Qy 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA 360

Db 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA 360

Qy 361 PVREEYADFKPFQAWVEVKDTEGSRDVLAAARANVESKVDRKCLEDSELEQKSLGKDSEGR 420

Db 361 PVREEYADFKPFQAWVEVKDTEGSRDVLAAARANVESKVDRKCLEDSELEQKSLGKDSEGR 420

Qy 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA 480

Db 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA 480

Qy 481 QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540

Db	481		QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Qy	541		NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Db	541		NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Qy	601		LPSAGASVVQPSVSPLEAPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Db	601		LPSAGASVVQPSVSPLEAPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Qy	661		NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Db	661		NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Qy	721		PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Db	721		PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Qy	781		NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Db	781		NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Qy	841		IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Db	841		IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Qy	901		DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED	960
Db	901		DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED	960
Qy	961		RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Db	961		RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Qy	1021		VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Db	1021		VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Qy	1081		FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA	1140
Db	1081		FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA	1140
Qy	1141		NKSVKDAMAKIQAKIPGLKRKAD	1163
Db	1141		NKSVKDAMAKIQAKIPGLKRKAD	1163

RESULT 2

AA71310

ID AAY71310 standard; Protein; 1163 AA.

XX

AC AAY71310;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo A.

XX
 KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening.

XX
 OS Rattus sp.

FH	Key	Location/Qualifiers
FT	Inhibitory-site	1..171
FT		/note= "Inhibits NIH 3T3 fibroblast spreading"
FT	Modified-site	30
FT		/note= "Casein kinase II site"
FT	Region	31..58
FT		/note= "Acidic region"
FT	Region	31..57
FT		/note= "Region specifically described in claim 16"
FT	Modified-site	233
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	242..244
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	291
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	295
FT		/note= "Protein kinase C (PKC) site"
FT	Misc-difference	404
FT		/note= "Encoded by TTG"
FT	Modified-site	436
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	468..470
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	484
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	488
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	502
FT		/note= "Casein kinase II site"
FT	Modified-site	576
FT		/note= "Casein kinase II site"
FT	Modified-site	626
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	694..696
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	715
FT		/note= "Casein kinase II site"
FT	Modified-site	784
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	821
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	850
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	855
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	863

FT /note= "Casein kinase II site"
 FT Modified-site 868
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 893
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 912..914
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 925..927
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 954
 FT /note= "PKC and casein kinase II sites"
 FT Modified-site 956
 FT /note= "PKC and casein kinase II sites"
 FT Domain 988..1023
 FT /label= Transmembrane_domain
 FT /note= "C-terminal hydrophobic region
 FT specifically described in claim 16"
 FT Modified-site 1024
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 1071..1073
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 1073
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 1089
 FT /note= "Protein kinase C (PKC) site"
 FT Domain 1090..1125
 FT /label= Transmembrane_domain
 FT /note= "C-terminal hydrophobic region
 FT specifically described in claim 16"
 FT Modified-site 1141..1143
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 1143
 FT /note= "Protein kinase C (PKC) site"
 FT Peptide 623..640
 FT /note= "used as immunogen to generate antibody AS 472"
 FT Peptide 762..1163
 FT /note= "used as immunogen to generate antibody AS Bruna"
 FT Inhibitory-site 542..722
 FT Region 172..259
 FT /note= "This region is not essential for inhibitory
 FT activity"
 FT Region 975..1162
 FT /note= "This region is not essential for inhibitory
 FT activity"
 FT Region 976..1163
 FT /note= "C-terminal common region found in Nogo A, B and
 FT C isoforms"
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US26160.
 XX
 PR 06-NOV-1998; 98US-0107446.
 XX
 PA (SCHW/) SCHWAB M E.

Db	121	PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAPPSTPAAPKRRGSGSVDETLFALP	180
Qy	181	AASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL	240
Db	181	AASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL	240
Qy	241	GNLSAVSSSEG TI EETLNEASKELPERATNP FVNRDLAEFSELEYSEMGS SFGSPKGES	300
Db	241	GNLSAVSSSEG TI EETLNEASKELPERATNP FVNRDLAEFSELEYSEMGS SFGSPKGES	300
Qy	301	AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA	360
Db	301	AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA	360
Qy	361	PVREEYADFKPF EQAWEVKD TYEGSRDVL AARANVESK VDRKCLED SLEQKSLGKDSEGR	420
Db	361	PVREEYADFKPF EQAWEVKD TYEGSRDVL AARANVESK VDRKCI EDSLEQKSLGKDSEGR	420
Qy	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA	480
Db	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA	480
Qy	481	QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Db	481	QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Qy	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Db	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Qy	601	LPSAGASVVQPSVSPLEAPPVSYDSIKLEPENPPPYEAMNVALKALGTKEG I KEPE SF	660
Db	601	LPSAGASVVQPSVSPLEAPPVSYDSIKLEPENPPPYEAMNVALKALGTKEG I KEPE SF	660
Qy	661	NAAVQETEAPYIS IACDLI KETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Db	661	NAAVQETEAPYIS IACDLI KETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Qy	721	PVDLFSDDSIPEVPQTQEEAVMLMKESL TEVSETVAQHKEERLSASPQELGKPYLESFQP	780
Db	721	PVDLFSDDSIPEVPQTQEEAVMLMKESL TEVSETVAQHKEERLSASPQELGKPYLESFQP	780
Qy	781	NLHSTKDAASNDIPTLT KKEKISLQMEEFNTAIYSNDDLLSSKEDKIKESETFS DSSPIE	840
Db	781	NLHSTKDAASNDIPTLT KKEKISLQMEEFNTAIYSNDDLLSSKEDKIKESETFS DSSPIE	840
Qy	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Db	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Qy	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED	960
Db	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED	960
Qy	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Db	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020

Qy 1021 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080
 |||||
 Db 1021 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080
 |||||
 Qy 1081 FLVDDLVDLKLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 1140
 |||||
 Db 1081 FLVDDLVDLKLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 1140
 |||||
 Qy 1141 NKSVKDAMAKIQAKIPGLKRKAD 1163
 |||||
 Db 1141 NKSVKDAMAKIQAKIPGLKRKAD 1163

RESULT 3

AAY71557

ID AAY71557 standard; Protein; 1162 AA.

XX

AC AAY71557;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat Nogo A truncated protein used in the construction of mutant Nogo-A.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; mutant; mutein.

XX

OS Rattus sp.

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US26160.

XX

PR 06-NOV-1998; 98US-0107446.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic
 PT disorders of the central nervous system and inducing regeneration of
 PT neurons -

XX

PS Example; Page -; 122pp; English.

XX

CC The patent relates to neurite growth inhibitor Nogo which is free of
 CC all central nervous system (CNS) myelin material with which it is

Db 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA 360

Qy 361 PVREEYADFKPFEQAWVEVKDITYEGSRDVLAAARANVESKVDRKCLEDSEQKSLGKDSEGR 420
 |||:|||||

Db 361 PVREEYADFKPFEQAWVEVKDITYEGSRDVLAAARANVESKVDRKCIEDSEQKSLGKDSEGR 420

Qy 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPILLEDHTSENKTDEKKIEERKA 480
 |||

Db 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPILLEDHTSENKTDEKKIEERKA 480

Qy 481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540
 |||

Db 481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540

Qy 541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600
 |||

Db 541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600

Qy 601 LPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEAMNVALKALGTKEGIKEPESF 660
 |||

Db 601 LPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEAMNVALKALGTKEGIKEPESF 660

Qy 661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720
 |||

Db 661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720

Qy 721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP 780
 |||

Db 721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP 780

Qy 781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE 840
 |||

Db 781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE 840

Qy 841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900
 |||

Db 841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900

Qy 901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED 960
 |||

Db 901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED 960

Qy 961 RLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 1020
 |||

Db 961 RLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 1020

Qy 1021 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080
 |||

Db 1021 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080

Qy 1081 FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 1140
 |||

Db 1081 FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 1140

Qy 1141 NKSVDAMAKIQAKIPGLKRKA 1162
 |||

Db 1141 NKSVDAMAKIQAKIPGLKRKA 1162

RESULT 4

AAY71384

ID AAY71384 standard; Protein; 1163 AA.

XX

AC AAY71384;

XX

DT 02-NOV-2000 (first entry)

XX

DE Alternative version of rat neurite growth inhibitor Nogo A.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Inhibitory-site 1..171

FT /note= "Inhibits NIH 3T3 fibroblast spreading"

FT Modified-site 30

FT /note= "Casein kinase II site"

FT Region 31..58

FT /note= "Acidic region"

FT Modified-site 233

FT /note= "Protein kinase C (PKC) site"

FT Modified-site 242..244

FT /note= "Asn is N-glycosylated"

FT Modified-site 291

FT /note= "Protein kinase C (PKC) site"

FT Modified-site 295

FT /note= "Protein kinase C (PKC) site"

FT Modified-site 436

FT /note= "Protein kinase C (PKC) site"

FT Modified-site 468..470

FT /note= "Asn is N-glycosylated"

FT Modified-site 484

FT /note= "Protein kinase C (PKC) site"

FT Modified-site 488

FT /note= "Protein kinase C (PKC) site"

FT Modified-site 502

FT /note= "Casein kinase II site"

FT Modified-site 576

FT /note= "Casein kinase II site"

FT Modified-site 626

FT /note= "Protein kinase C (PKC) site"

FT Modified-site 694..696

FT /note= "Asn is N-glycosylated"

FT Modified-site 715

FT /note= "Casein kinase II site"

FT Modified-site 784

FT /note= "Protein kinase C (PKC) site"

FT	Modified-site	821
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	850
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	855
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	863
FT		/note= "Casein kinase II site"
FT	Modified-site	868
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	893
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	912..914
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	925..927
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	954
FT		/note= "PKC and casein kinase II sites"
FT	Modified-site	956
FT		/note= "PKC and casein kinase II sites"
FT	Domain	988..1023
FT		/label= Transmembrane_domain
FT		/note= "C-terminal hydrophobic region"
FT	Modified-site	1024
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	1071..1073
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	1073
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	1089
FT		/note= "Protein kinase C (PKC) site"
FT	Domain	1090..1125
FT		/label= Transmembrane_domain
FT		/note= "C-terminal hydrophobic region"
FT	Modified-site	1141..1143
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	1143
FT		/note= "Protein kinase C (PKC) site"
FT	Peptide	623..640
FT		/note= "used as immunogen to generate antibody AS 472"
FT	Peptide	762..1163
FT		/note= "used as immunogen to generate antibody AS Bruna"
FT	Inhibitory-site	542..722
FT	Region	172..259
FT		/note= "This region is not essential for inhibitory activity"
FT	Region	975..1162
FT		/note= "This region is not essential for inhibitory activity"
FT	Region	976..1163
FT		/note= "C-terminal common region found in Nogo A, B and C isoforms"
FT	Misc-difference	223
FT		/label= Unknown
FT		/note= "There is Leu at this position in the sequence shown in AAY71310"
FT	Misc-difference	404

FT /note= "There is Ile at this position in the
 FT sequence shown in AAY71310"
 FT Misc-difference 469
 FT /label= Unknown
 FT /note= "There is Lys at this position in the
 FT sequence shown in AAY71310"
 FT Misc-difference 661
 FT /note= "There is Asn at this position in the
 FT sequence shown in AAY71310"
 FT Misc-difference 820
 FT /note= "There is Leu at this position in the
 FT sequence shown in AAY71310"
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US26160.
 XX
 PR 06-NOV-1998; 98US-0107446.
 XX
 PA (SCHW/) SCHWAB M E.
 PA (CHEN/) CHEN M S.
 XX
 PI Schwab ME, Chen MS;
 XX
 DR WPI; 2000-400052/34.
 XX
 PT Nogo proteins and nucleic acids useful for treating neoplastic
 PT disorders of the central nervous system and inducing regeneration of
 PT neurons -
 XX
 PS Claim 3; Fig 13; 122pp; English.
 XX
 CC The present sequence is an alternative version of rat Nogo A protein
 CC which is a potent neural cell growth inhibitor and is free of all
 CC central nervous system (CNS) myelin material with which it is
 CC natively associated. Nogo proteins and fragments displaying
 CC neurite growth inhibitory activity are used in the
 CC treatment of neoplastic disease of the CNS
 CC e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
 CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
 CC Therapeutics which promote Nogo activity can be used to treat or prevent
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
 CC used to inhibit production of Nogo protein to induce regeneration of
 CC neurons or to promote structural plasticity of the CNS in disorders where
 CC neurite growth, regeneration or maintenance are deficient or desired.
 CC The animal models can be used in diagnostic and screening methods for
 CC predisposition to disorders and to screen for or test molecules which
 CC can treat or prevent disorders or diseases of the CNS.
 CC Note: The present sequence is an alternative version of the
 CC Nogo A sequence shown in Fig. 2A (see AAY71310).
 CC SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29
 CC in disclosure of the specification. However the specification does not

CC include sequences for these SEQ ID numbers.

XX

SQ Sequence 1163 AA;

Query Match 99.6%; Score 5823; DB 21; Length 1163;
Best Local Similarity 99.7%; Pred. No. 2.1e-295;
Matches 1159; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy      1 MEDIDQSSLVSSSTDSPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEELVLERK 60
      |||
Db      1 MEDIDQSSLVSSSTDSPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEELVLERK 60

Qy     61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
      |||
Db     61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120

Qy    121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPSTPAAPKRRGSGSVDETLFALP 180
      |||
Db    121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPSTPAAPKRRGSGSVDETLFALP 180

Qy    181 AASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240
      |||
Db    181 AASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASXPSLSPLSTVSFKEHGYL 240

Qy    241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSFSGSPKGES 300
      |||
Db    241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSFSGSPKGES 300

Qy    301 AILVENTKEEVIVRSKDEDLVCSAALHSPQESFVGKEDRVVSPEKTMDIFNEMQMSVVA 360
      |||
Db    301 AILVENTKEEVIVRSKDEDLVCSAALHSPQESFVGKEDRVVSPEKTMDIFNEMQMSVVA 360

Qy    361 PVREEYADFKPFQAWVEKDTYEGSRDVLAAARANVESKVDRKCLEDLSLEQKSLGKDSEGR 420
      |||
Db    361 PVREEYADFKPFQAWVEKDTYEGSRDVLAAARANVESKVDRKCLEDLSLEQKSLGKDSEGR 420

Qy    421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLEDHTSENKTDEKKIEERKA 480
      |||
Db    421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLEDHTSENXTDEKKIEERKA 480

Qy    481 QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540
      |||
Db    481 QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540

Qy    541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600
      |||
Db    541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600

Qy    601 LPSAGASVVQPSVSPLEAPPPVSYSYDIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF 660
      |||
Db    601 LPSAGASVVQPSVSPLEAPPPVSYSYDIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF 660

Qy    661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720
      |||
Db    661 MAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720

Qy    721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQP 780
```

Db	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Qy	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Db	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Qy	841	IIDEFPPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Db	841	IIDEFPPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Qy	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED	960
Db	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED	960
Qy	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Db	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Qy	1021	VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Db	1021	VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Qy	1081	FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGIA	1140
Db	1081	FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGIA	1140
Qy	1141	NKSVKDAMAKIQAKIPGLKRRKAD	1163
Db	1141	NKSVKDAMAKIQAKIPGLKRRKAD	1163

RESULT 5

AAY71560

ID AAY71560 standard; Protein; 974 AA.

XX

AC AAY71560;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat Nogo A protein fragment used in the construction of mutant NiAext.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; mutant; mutein.

XX

OS Rattus sp.

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US26160.

```

XX
PR 06-NOV-1998; 98US-0107446.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic
PT disorders of the central nervous system and inducing regeneration of
PT neurons -
XX
PS Example; Page -; 122pp; English.
XX
CC The patent relates to neurite growth inhibitor Nogo which is free of
CC all central nervous system (CNS) myelin material with which it is
CC natively associated. Nogo proteins and fragments displaying neurite
CC growth inhibitory activity are used in the treatment of neoplastic
CC disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,
CC craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic
CC neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma
CC and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
CC diseases. Therapeutics which promote Nogo activity can be used to treat
CC or prevent hyperproliferative or benign dysproliferative disorders e.g.
CC psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic
CC acids can be used to inhibit production of Nogo protein to induce
CC regeneration of neurons or to promote structural plasticity of the CNS
CC in disorders where neurite growth, regeneration or maintenance are
CC deficient or desired. The animal models can be used in diagnostic and
CC screening methods for predisposition to disorders and to screen for or
CC test molecules which can treat or prevent disorders or diseases of the
CC CNS. The present sequence is a fragment of rat Nogo A protein shown in
CC AAY71310, which is used in the construction of mutant NiAext. The mutant
CC is composed of His-tag/T7-tag/vector/Nogo-A sequence aa 1-974/T7-tag.
CC Nogo A deletion mutants were used for mapping the inhibitory sites of
CC Nogo protein. Major inhibitory region was identified in the
CC Nogo A sequence from amino acids 172-974, particularly amino acids
CC 542-722. In addition, N-terminal region 1-171 was found to be inhibitory
CC to NIH 3T3 fibroblast spreading.
CC Note: The present sequence is not given in the specification but is
CC derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42
CC are referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However, the specification does not include sequences for
CC these SEQ ID numbers.
XX
SQ Sequence 974 AA;

Query Match 84.1%; Score 4921; DB 21; Length 974;
Best Local Similarity 99.9%; Pred. No. 1.9e-248;
Matches 973; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
   |||||
Db 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60

```

Qy	61	PAAGLSAAAVPPAAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP	120
Db	61	PAAGLSAAAVPPAAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP	120
Qy	121	PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAAPPSTPAAPKRRGSGSVDETLFALP	180
Db	121	PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAAPPSTPAAPKRRGSGSVDETLFALP	180
Qy	181	AASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL	240
Db	181	AASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL	240
Qy	241	GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSEFKGSPKGES	300
Db	241	GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSEFKGSPKGES	300
Qy	301	AILVENTKEEVI VRSKDKEDLVCSAALHSPQESVPGKEDRVVSPEKTMDFNEMQMSVVA	360
Db	301	AILVENTKEEVI VRSKDKEDLVCSAALHSPQESVPGKEDRVVSPEKTMDFNEMQMSVVA	360
Qy	361	PVREEYADFKPFQAWVEVKDITYEGSRDVLAAARANVESKVDKRCLEDSLEQKSLGKDSEGR	420
Db	361	PVREEYADFKPFQAWVEVKDITYEGSRDVLAAARANVESKVDKRCIEDSLEQKSLGKDSEGR	420
Qy	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPILLEDHTSENKTDEKKIEERKA	480
Db	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPILLEDHTSENKTDEKKIEERKA	480
Qy	481	QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Db	481	QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Qy	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Db	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Qy	601	LPSAGASVVQPSVSPLEAPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Db	601	LPSAGASVVQPSVSPLEAPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Qy	661	NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Db	661	NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Qy	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Db	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Qy	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Db	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Qy	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLLPCDLSFKNIYPK	900
Db	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLLPCDLSFKNIYPK	900
Qy	901	DEVHVSDEFSENRRSSVSKASISPSNVSALEPQTEMGSIIVKSKSLTKEAEKKLPSDTEKED	960

```

Db      901 DE|V|H|V|S|D|E|F|S|E|N|R|S|S|V|S|K|A|S|I|S|P|S|N|V|S|A|L|E|P|Q|T|E|M|G|S|I|V|K|S|K|S|L|T|K|E|A|E|K|K|L|P|S|D|T|E|K|E|D 960
Qy      961 R|S|L|S|A|V|L|S|A|E|L|S|K|T 974
Db      961 R|S|L|S|A|V|L|S|A|E|L|S|K|T 974

```

RESULT 6

AAU04591

ID AAU04591 standard; Protein; 1192 AA.

XX

AC AAU04591;

XX

DT 26-SEP-2001 (first entry)

XX

DE Human Nogo protein.

XX

KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;
KW cranial trauma; cerebral trauma; spinal cord injury; stroke;
KW demyelinating disease; multiple sclerosis; monophasis demyelination;
KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;
KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;
KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;
KW Canavan's disease; metachromatic leukodystrophy; viral infection;
KW Krabbe's disease.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	Domain	1054..1119
FT		/label= Lumenal_extracellular_domain
FT		/note= "This sequence is specifically claimed"
FT	Peptide	1055..1094
FT		/label= Pep1
FT		/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"
FT	Peptide	1064..1088
FT		/label= Pep2
FT		/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"
FT	Peptide	1074..1098
FT		/label= Pep3
FT		/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"
FT	Peptide	1084..1108
FT		/label= Pep4
FT		/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"
FT	Peptide	1095..1119
FT		/label= Pep5
FT		/note= "Receptor binding inhibitory peptide. This sequence is specifically claimed"

XX

PN WO200151520-A2.

XX

PD 19-JUL-2001.


```

XX      12-JAN-2001; 2001WO-US01041.
XX
PR      12-JAN-2000; 2000US-0175707.
PR      26-MAY-2000; 2000US-0207366.
PR      29-SEP-2000; 2000US-0236378.
XX
PA      (UYYA ) UNIV YALE.
XX
PI      Strittmatter SM;
XX
DR      WPI; 2001-442138/47.
DR      N-PSDB; AAS09453.
XX
PT      Novel Nogo receptor protein useful for identifying modulator of Nogo
PT      protein or Nogo receptor protein, which is useful for treating central
PT      nervous system disorders  -
XX
PS      Example 1; Page 101-104; 109pp; English.
XX
CC      The sequence is the human Nogo protein, a 250kDa myelin-associated axon
CC      growth inhibitor. The invention relates to the use of the nogo receptor,
CC      nogo protein, their nucleic acids, vectors expressing them and antibodies
CC      against them, to isolate agents which block nogo receptor mediated axonal
CC      growth. The agent is useful for treating a central nervous system
CC      disorder which is a result of cranial or cerebral trauma, spinal cord
CC      injury, stroke or a demyelinating disease selected from multiple
CC      sclerosis, monophasis demyelination, encephalomyelitis, multifocal
CC      leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease,
CC      pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease,
CC      Spongy degeneration, Alexander's disease, Canavan's disease,
CC      metachromatic leukodystrophy, viral infection and Krabbe's disease.
XX
SQ      Sequence      1192 AA;

Query Match          75.3%;  Score 4403.5;  DB 22;  Length 1192;
Best Local Similarity 75.9%;  Pred. No. 2.5e-221;
Matches 909;  Conservative 104;  Mismatches 145;  Indels 39;  Gaps 20;

QY      1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEELEVLERK 60
      |||:|||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      1 MEDLDQSPLVSSS-DSPRRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK 58

QY      61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
      ||||| || || ||| |||:| | ||||| ||||| ||||| ||||| ||| : |
DB      59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVP 118

QY      116 APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
      ||| |||| ||||| ||||| ||||| ||||| || || ||||| |||||
DB      119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPAPAPAAPSTPAAPKR 178

QY      167 RG-SGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
      || ||||| ||||| ||||| |||| ||||| ||||| ||||| ||||| |||||
DB      179 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237

QY      226 LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285
      ||||| ||||| ||||| ||| :|||:| :|||:| :| :||| |||||

```

Db 238 LSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297

Qy 286 SEMGSSFKGSPKGESAILVENTKEEVI VRSKDKED-LVCSAALHSPQESPVG-----KED 339
 ||||| ||| ||:| | :||:|:|:|:| | : ||: || | |||

Db 298 SEMGSSFSVSPKAESAVIVANPREEI I VKNKDEEEKLVSNNILHNQQELPTALTCLKVKED 357

Qy 340 RVVSPEKTMDIFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANV 395
 ||| || | ||| :| | :||| |||||: ||||: | | |:| | :|:

Db 358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy 396 ESKVDRKCLEDSLEQKSLGKDSGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
 ||||:| | |||| : |||| |:| ||||| :|| | ||||| | :|||

Db 417 ESKVDDKKCFADSLEQTNHEKDSSESSNDTSFPSTPEGIKDRSGAYITCAPFNPAAATESIA 476

Qy 455 ANTFPILLEDHTSENKTDEKKIEERKAQI I TEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
 | |||| | ||||| |||||: |||: || | ||||| |||| | |||| |:

Db 477 TNIFPLLGDPTSENKTDEKKIEEKAQI VTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 536

Qy 514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573
 |||| |:| ||||| ||||| ||||| |||||: ||||| |||

Db 537 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL 596

Qy 574 CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPEN 633
 |||||: ||||| ||||| ||||| : |||||: ||| |||| |:|: ||| |||

Db 597 CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPEN 655

Qy 634 PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDF 692
 |||||:|:|:| | : | || ||||: ||:| ||||| ||||| ||||| ||:|

Db 656 PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDF 715

Qy 693 SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS 752
 |:|:|:| | |: |:|:| |||||: ||||| |||||: ||| |:| |:|:| |||| |

Db 716 SDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETS 775

Qy 753 -ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF 809
 |:|:|:| |:|:| | | |||||: |:|:| | :|:| |:|:| ||||

Db 776 FESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEEL 835

Qy 810 NTAIYNSDDLSSKEDKIKESETFSDSSPIEI I DEFPTFVSAKDDS-PKLAKEYTDLEVS 868
 |:|:| |||| | || |:|:| ||||| ||||| |:| | | |:|:| ||||

Db 836 STAVYNSDDLFIKSEAQIRETETFSDDSPIEI I DEFPTLISSKTDSFSKLAREYTDLEVS 895

Qy 869 DKSEIANIQSGADSLPCLLELPDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV 926
 ||||| || | |||| ||| ||| ||| ||| :|:| |:|:| |:| | :|:|

Db 896 HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDPV 955

Qy 927 SALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986
 ||| | |:| ||| | | ||||| ||||| |:| ||||| ||||| |||||

Db 956 SALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK 1015

Qy 987 KTGUVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRA 1046
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1016 KTGUVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRA 1075

Qy 1047 YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF 1106
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1076 YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF 1135

OS Homo sapiens.
 XX
 PN WO200005364-A1.
 XX
 PD 03-FEB-2000.
 XX
 PF 21-JUL-1999; 99WO-GB02360.
 XX
 PR 22-JUL-1998; 98GB-0016024.
 PR 19-JUL-1999; 99GB-0016898.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Michalovich D, Prinjha RK;
 XX
 DR WPI; 2000-182693/16.
 DR N-PSDB; AAZ56886.
 XX
 PT Novel polypeptides related to neuroendocrine-specific proteins and
 PT polynucleotides useful for diagnosis of various diseases and for
 PT treatment of cancer and neurological disorders -
 XX
 PS Claim 2; Page 20-21; 35pp; English.
 XX
 CC The invention relates to human MAGI protein, which is similar to
 CC neuroendocrine-specific protein. The MAGI protein can be expressed by
 CC standard recombinant methodology. The MAGI polypeptides, polynucleotides
 CC and antibodies are useful for treating diseases, including neuropathies,
 CC spinal injury, neuronal degeneration, neuromuscular disorders,
 CC psychiatric disorders and developmental disorders, cancer, stroke and
 CC inflammatory disorders. The polynucleoitde is also useful for chromosome
 CC localization and for tissue expression studies. The present sequence
 CC represents the human MAGI protein.
 XX
 SQ Sequence 1192 AA;

Query Match 75.2%; Score 4398.5; DB 21; Length 1192;
 Best Local Similarity 75.9%; Pred. No. 4.5e-221;
 Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;

Qy 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
 |||:||||| ||||| ||||| ||||| ||||| |||||:|:|:|||||
 Db 1 MEDLDQSPLVSSS-DSPPRQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEEVLERK 58
 Qy 61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
 ||||| || ||| |||:| :| ||||| ||||| |||||: || : |
 Db 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSSTVP 118
 Qy 116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
 ||| ||| ||||| ||||| ||||| || || |||||
 Db 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPAPAPAAPPSTPAAPKR 178
 Qy 167 RG-SGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
 || ||||| ||||| ||||| ||| |||||:|:|:|||||
 Db 179 RGSSGSVDETLFALPAASEPVI RSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237
 Qy 226 LSPLSTVSFKEHG YLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285

Db 238 LSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297
 Qy 286 SEMGSSFKGSPKGESAILVENTKEEVI VRSKDKED-LVCSAALHSPQESPVG-----KED 339
 Db 298 SEMGSSFSVSPKAESAVIVANPREEIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKED 357
 Qy 340 RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANV 395
 Db 358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416
 Qy 396 ESKVDRKCLEDSLEQKSLGKDSSEGRNEDASFPSTPEPVKDSRAYITCASFT-SATESTT 454
 Db 417 ESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIA 476
 Qy 455 ANTFPILLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
 Db 477 TNIFPLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 536
 Qy 514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573
 Db 537 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL 596
 Qy 574 CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPEN 633
 Db 597 CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPEN 655
 Qy 634 PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDF 692
 Db 656 PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDF 715
 Qy 693 SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS 752
 Db 716 SDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMLVKESLTETS 775
 Qy 753 -ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF 809
 Db 776 FESMIEYENKEKLSALPPEGGKPYLESFKLSLNTKDTLLPDEVSTLSKKEKIPLOMEEL 835
 Qy 810 NTAIYSNDDLSSKEDKIKESETFSDSSPIEIDEFPFVSADKDS-PKLAKEYTDLEVS 868
 Db 836 STAVYSNDDLFIKSEAQIRETETFSDDSSPIEIDEFPFLISSKTDSPSKLAREYTDLEVS 895
 Qy 869 DKSEIANIQSGADSLPCLSLFKNIPYK--DEVHVSDEFSENRRSSVSKASISPSNV 926
 Db 896 HKSEIANAPDGAGSLPCTELPHDLSLKNIPKVEEKISFSDDFSKNGSATSKVLLLPDV 955
 Qy 927 SALEPQTEMGSIKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986
 Db 956 SALATQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK 1015
 Qy 987 KTGUVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA 1046
 Db 1016 KTGUVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA 1075
 Qy 1047 YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALF 1106

Db	656	PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDF	715
Qy	693	SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS	752
Db	716	SDYSEMAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETS	775
Qy	753	-ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF	809
Db	776	FESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEEL	835
Qy	810	NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVS	868
Db	836	STAVYSNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLSSKTDTSFKLAREYTDLEVS	895
Qy	869	DKSEIANIQSGADSLPCLSLPCDLFSKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV	926
Db	896	HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNKSATSKVLLLPDPV	955
Qy	927	SALEPQTEMGSIVKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK	986
Db	956	SALATQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK	1015
Qy	987	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHFPRA	1046
Db	1016	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHFPRA	1075
Qy	1047	YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1106
Db	1076	YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1135
Qy	1107	NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD	1163
Db	1136	NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 10

ABB81078

ID ABB81078 standard; Protein; 1192 AA.

XX

AC ABB81078;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human neurotransmitter receptor protein Nogo-A.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
 KW neurotransmitter receptor; human; receptor.

XX

OS Homo sapiens.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.
 XX
 PF 28-JUN-2001; 2001US-0893348.
 XX
 PR 19-MAY-1998; 98IL-0124500.
 PR 21-JUL-1998; 98WO-US14715.
 PR 22-DEC-1998; 98US-0218277.
 PR 19-MAY-1999; 99US-0314161.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
 PI Moalem G;
 XX
 DR WPI; 2002-607255/65.
 DR N-PSDB; ABN86601.
 XX
 PT Promoting nerve regeneration and preventing neuronal degeneration in
 PT the central/peripheral nervous system from injury/disease, comprises
 PT administering nervous system-specific activated T cells/antigen, or
 PT analogs/peptides -
 XX
 PS Examples; Page 53-56; 93pp; English.
 XX
 CC The invention relates to promoting nerve regeneration or conferring
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the
 CC central/peripheral nervous system (NS). The method involves administering
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
 CC combinations. The method is useful for promoting nerve regeneration and
 CC preventing neuronal degeneration in central/peripheral nervous system
 CC from injury/disease, where the injury is spinal cord injury, blunt
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
 CC damages caused by surgery such as tumour excision. The disease is not an
 CC autoimmune disease or neoplasm. The disease results in a degenerative
 CC process occurring in either gray or white matter or both. The disease
 CC is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
 CC neuropathies associated with various diseases, including but not limited
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
 CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
 CC disease, or lipoproteinemia. The present sequence represents the human
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific
 CC antigen.
 XX
 SQ Sequence 1192 AA;

Query Match

75.2%; Score 4398.5; DB 23; Length 1192;

Db	776	FESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOQMEEL	835
Qy	810	NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIIDEFPTFVSAKDDS-PKLAKEYTDLEVS	868
Db	836	STAVYSNDDLFI SKEAQIRETETFS DSSPIEIIIDEFPTLISSKTD SFSKLAREYTDLEVS	895
Qy	869	DKSEIANIQSGADSLPCLELPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV	926
Db	896	HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDPV	955
Qy	927	SALEPQTEMGSI VSKSLTKEAEKKLPSPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK	986
Db	956	SALATQAEIESIVKPKVLVKEAEKKLPSPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK	1015
Qy	987	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1046
Db	1016	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1075
Qy	1047	YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1106
Db	1076	YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1135
Qy	1107	NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD	1163
Db	1136	NGLTLLILALISLFSVPVIYERHOAOIDHYLGLANKNVKDAMAKIOAKIPGLKRKAE	1192

RESULT 11
ABG30938
ID ABG30938 standard; Protein; 1192 AA.
XX
AC ABG30938;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human NogoA protein.
XX
KW Human; Nogo; BACE; acute neuronal in
KW stroke; peripheral nerve damage; neo
KW neuroblastoma; hyperproliferative di
KW cirrhosis; psoriasis; keloid formati
KW tissue hypertrophy; central nervous
KW Nogo-associated disease; metastasis.
XX
OS Homo sapiens.
XX
PN WO200257483-A2.
XX
PD 25-JUL-2002.
XX
PF 18-JAN-2002; 2002WO-GB00228.
XX
PR 18-JAN-2001; 2001GB-0001312.
XX
PA (GLAX) GLAXO GROUP LTD.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX

PI Blackstock WP, Hale RS, Prinjha R, Rowley A;

XX

DR WPI; 2002-599722/64.

DR N-PSDB; ABK90134.

XX

PT Identifying modulators of Nogo or BACE activity for treating acute
PT neuronal injuries, neoplastic or dysproliferative disorders, comprises
PT providing and monitoring interaction between Nogo and BACE polypeptides

PT -

XX

PS Disclosure; Page 59-62; 68pp; English.

XX

CC The present invention relates to a new method of identifying modulators
CC of Nogo function or BACE activity. The method involves providing Nogo and
CC BACE polypeptides capable of binding with each other, monitoring the
CC interaction between these polypeptides, and determining if the test agent
CC is a modulator of Nogo or BACE activity. The method is useful in treating
CC acute neuronal injuries, such as spinal or head injury, stroke,
CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,
CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.
CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue
CC hypertrophy) of the central nervous system. The BACE polypeptide is
CC useful in screening methods to identify agents that may act as modulators
CC of BACE activity and in particular agents that may be useful in treating
CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,
CC and the polynucleotide encoding the BACE polypeptide are useful in
CC manufacturing a medicament for the treatment or prevention of disorders
CC responsive to the modulation of Nogo activity, in alleviating the
CC symptoms or improving the condition of a patient suffering from this
CC disorder, in axon regeneration, or in preventing metastasis or spreading
CC of a cancer. The polynucleotide may also be an essential component in
CC assays, a probe, in recombinant protein synthesis, and in gene therapy
CC techniques. The present amino acid sequence represents the human NogoA
CC protein of the invention.

XX

SQ Sequence 1192 AA;

Query Match 75.2%; Score 4398.5; DB 23; Length 1192;

Best Local Similarity 75.9%; Pred. No. 4.5e-221;

Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;

```
Qy      1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLLEEVLERK 60
      |||:|||| ||||| ||||| ||||| ||||| |||||:|:|:|||||
Db      1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLLEEVLERK 58

Qy     61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
      ||||| || || |||:| | :| ||||| ||||| |||||: || : |
Db     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVP 118

Qy    116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
      ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178

Qy    167 RG-SGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
      || ||||| ||||| ||||| ||||| |||||:|:|||||
Db    179 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237
```

Qy 226 LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285
 ||||| ||||| ||||| | :|||::| :||| ||||| :||| :||| ||||| |||||
 Db 238 LSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297

Qy 286 SEMGSSFKGSPKGESAILVENTKEEVI VRSKDKED-LVCSAALHSPQESPVG-----KED 339
 ||||| ||| |||::| | :||:|::|:|:| | | : ||: || | |||
 Db 298 SEMGSSFSVSPKAESAVIVANPREEI I VKNKDEEEKLVSNNILHNQQELPTALTCLKVKED 357

Qy 340 RVVSPEKTMDFNEMQMSVVPVREEYADFKPFQAWEVKDTYEGSRDVLAA----RANV 395
 ||| || | ||| :::| ||:|||||||: ||||: | | |:||| :||:
 Db 358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy 396 ESKVDRKCLEDSELEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
 |||||:|| ||||| : |||| |:| ||||| :|| ||||| | :|||
 Db 417 ESKVDDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAAATESIA 476

Qy 455 ANTFPILLEDHTSENKTDEKKIEERKAQI I TEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
 | |||| | ||||| |||||:|||||: ||| || ||||| ||||| ||||| :|
 Db 477 TNIFPLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 536

Qy 514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573
 |||| |:||||||||||||||||| |||||:|||||: ||||| ||||| |||||
 Db 537 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL 596

Qy 574 CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQSPVPLEAPPVSYDSIKLEPEN 633
 |||||:||||||||||||||||| :|||||:||| |||| |:|:||| ||||
 Db 597 CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPEN 655

Qy 634 PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDF 692
 |||||:|:| | : | || ||||: |||:||||||||||||||||| ||:|
 Db 656 PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDF 715

Qy 693 SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS 752
 |:|:|:| |: |:|:|:|||||:|||||:| | |:| |:|:|:| |
 Db 716 SDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS 775

Qy 753 -ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF 809
 |:|:|:| |:|:| | | |||||: |:| :||| ::: ||:| ||||| |||||
 Db 776 FESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEEL 835

Qy 810 NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVS 868
 :|:|:| ||| |:|:|:|||||:|||||:|:| || |:|:|:|
 Db 836 STAVYSNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVS 895

Qy 869 DKSEIANIQSGADSLPCLLPCLDSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV 926
 ||||| || |||| ||| ||| ||| ||| ::: ||:|:| |:| | :|:
 Db 896 HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVVLLLPDPV 955

Qy 927 SALEPQTEMGSIVKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986
 ||| | |: ||| | | ||||| ||||| |||: ||||| ||||| |||||
 Db 956 SALATQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK 1015

Qy 987 KTG VVFGASL FLLLSLT VFSI VSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRA 1046
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1016 KTG VVFGASL FLLLSLT VFSI VSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRA 1075

Qy 1047 YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALF 1106

```

Db      1076 YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVLMWVFTYVGALF 1135
Qy      1107 NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
Db      1136 NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

```

RESULT 12

AAY71311

ID AAY71311 standard; Protein; 1178 AA.

XX

AC AAY71311;

XX

DT 02-NOV-2000 (first entry)

XX

DE Human neurite growth inhibitor Nogo.

XX

KW Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Misc-difference	187
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	188
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	189
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	190
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	221
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	328
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	477
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Region	994..1174
----	--------	-----------

FT		/note= "Region specifically described in claim 16"
----	--	----------------------------------------------------

FT	Region	977..1012
----	--------	-----------

FT		/note= "Region specifically described in claim 16"
----	--	----------------------------------------------------

FT	Region	1079..1114
----	--------	------------

FT		/note= "Region specifically described in claim 16"
----	--	----------------------------------------------------

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US26160.

XX

PR 06-NOV-1998; 98US-0107446.

XX (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic
PT disorders of the central nervous system and inducing regeneration of
PT neurons -
XX
PS Claim 11; Fig 13; 122pp; English.
XX
CC The present sequence is a human Nogo protein which is a
CC potent neural cell growth inhibitor and is free of all central nervous
CC system (CNS) myelin material with which it is natively associated. The
CC human Nogo sequence was derived by aligning human expressed sequence tags
CC (ESTs) e.g. AA158636, AA333267, AA081783, AA167765, AA322918, AA092565,
CC AA081525 and AA081840 with the rat Nogo sequence.
CC Nogo proteins and fragments displaying neurite growth inhibitory
CC activity are used in the treatment of neoplastic disease of the CNS
CC e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
CC menagioma, neuroblastoma or retinoblastoma and degenerative nerve
CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
CC promote Nogo activity can be used to treat or prevent hyperproliferative
CC or benign dysproliferative disorders e.g. psoriasis and tissue
CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
CC inhibit production of Nogo protein to induce regeneration of neurons or
CC to promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired.
CC The animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which
CC can treat or prevent disorders or diseases of the CNS.
CC Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29
CC in disclosure of the specification. However the specification does not
CC include sequences for these SEQ ID numbers.
XX
SQ Sequence 1178 AA;

Qy	1	MEDIDQSSLVSSSTDSPRP	PPPAFKYQFVTEPEDEE	EEEEEEEEDEEDEDLEEL	EVLERK	60
		:		: :		
Db	1	MEDLDQSPLVSS-DSVPR	PQPAFKYQFVREPEDEE	-EEEEEEEEDEEDEDLEEL	EVLERK	58
				: :		
Qy	61	PAAGLSAAAVP--PAA	AAPLLDFSSDSVP	PAPRGPLPAAPPAAPER	QPSWERSPAA---P	115
			: :		: :	
Db	59	PAAGLSAAPVPTA	PAGAPLMDFGNDFV	PAPRGPLPAAPPVAPER	QPSWDPSPVSSTVP	118
					: :	
Qy	116	APSLPPAAAVLPSKL	PEDEPPARPPPPPP	PAGASPLAE-----	PAAPPSTPAAPKR	166
Db	119	APSPLSAAAVSPSKL	PEDEPPARPPPPPP	PASVSPOAEPVWTP	PAPAPAAPSTPAAPKR	178

Qy 167 RSGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL 226
 ||| : ||||| |||||:|:||||| ||||| |||
 Db 179 RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL 224

Qy 227 SPLSTVSFKEHGYLGNL SAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYS 286
 |||| | |||| | |||| | :|||:| :|||:| :| :| :||| ||||| |||
 Db 225 SPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS 284

Qy 287 EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR 340
 ||||| ||| |||:| | :||:|:|:|:| | : || || | |||
 Db 285 EMGSSFSVSPKAESAVIVANPREEII VKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDE 344

Qy 341 VVSPEKTMDIFNEMQMSV VAPVREEYADFKPFQAWEVKDTYEGSRDVLAA----RANVE 396
 ||| || | ||| :||| | ||:|||||||: ||||: | | :||| :|:|
 Db 345 VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE 403

Qy 397 SKVDRKCLED SLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTTA 455
 ||||:| | |||| : ||| | :| ||||| :| | ||||| | :|||
 Db 404 SKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT 463

Qy 456 NTFPLLEDHTSENKTDEKKIEERKAQI I TEK-TSPKTSNPFLVAVQDSEADYVTTDTLSK 514
 | ||||| |||| | |||||:|||:| | ||||| || ||| ||||| |:|
 Db 464 NIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSCTDYVTTDNLT 523

Qy 515 VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLC 574
 ||| |:||||| ||||| ||||| |||||: ||||| : ||||| |||||
 Db 524 VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLC 583

Qy 575 PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENP 634
 ||||:||||| ||||| ||||| : |||||: ||| |||| |:|: ||| |||||
 Db 584 PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESI KHPEPENP 642

Qy 635 PPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDFSN 694
 |||||:|:| | | ||||: |||:||||| ||||| ||||| |||||:|:|
 Db 643 PPYEEAMSVSLKVGSIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSD 702

Qy 695 YSEIAKFEKSVPEHAELVEDSSPESEPVDFSDDSIPEVPQTQEEAVMLMKESLTEVS-E 753
 |||:| |: |:|:|||||: ||||| |||||: ||| |:| |||: ||||| | |
 Db 703 YSEMAKVEQPVPDHSELVEDSSPDSEPVDFSDDSIPDVPQKQDETVM LVKESLTETSFE 762

Qy 754 TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT 811
 :: :: :|:| | | |||||: :| :||| ::: ||: |||| | ||| :|
 Db 763 SMIEYENKEKLSALPPEGGKPYLESFKLSLVNTKDTLLPDEVSTLSKKEKIPLOMEELST 822

Qy 812 AIYSNDDLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVSDK 870
 |:| |||| ||| :|:|:||||| ||||| ||||| :|:| || |:| ||||| |
 Db 823 AVYSNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLSSKTDSFSKLAREYTDLEVSHK 882

Qy 871 SEIANIQSGADSLPCLLPCLDSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNVSA 928
 |||| | |||| ||| ||| ||| ||| ::: |:|:| |:| | :|:| |
 Db 883 SEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSA 942

Qy 929 L-EPQTEMGSI VSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK 987
 | |: ||| | | ||||| ||||| |||: ||| | ||||| |||||
 Db 943 LGHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKK 1002

Qy 988 TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY 1047

```

      |||
Db      1003 TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAIQKSDEGHPFRAY 1062
      |||
Qy      1048 LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLKFVLMWVFTYVGALFN 1107
      |||
Db      1063 LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVLMWVFTYVGALFN 1122
      |||
Qy      1108 GLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
      |||
Db      1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178

```

RESULT 13

AAU33228

ID AAU33228 standard; Protein; 1246 AA.

XX

AC AAU33228;

XX

DT 18-DEC-2001 (first entry)

XX

DE Novel human secreted protein #3719.

XX

KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX

OS Homo sapiens.

XX

PN WO200179449-A2.

XX

PD 25-OCT-2001.

XX

PF 16-APR-2001; 2001WO-US08656.

XX

PR 18-APR-2000; 2000US-0552929.

PR

26-JAN-2001; 2001US-0770160.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-611725/70.

XX

PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -

XX

PS Claim 20; Page 737; 765pp; English.

XX

CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically

CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.

XX

SQ Sequence 1246 AA;

Query Match 70.4%; Score 4116; DB 22; Length 1246;
 Best Local Similarity 72.0%; Pred. No. 2.6e-206;
 Matches 873; Conservative 112; Mismatches 171; Indels 56; Gaps 27;

```

Qy      1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
      |||:||||| ||||| ||||| ||||| ||||| |||||:|:| ||||| |||||
Db      42 MEDLDQSPLVSSS-DSPRRQPAPFKYQFVREPEDEE-EEEEEEEEDEDEDLEEEVLERK 99

Qy      61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
      ||||| ||| ||| |||:| | :| ||||| ||||| ||||| ||| : |
Db     100 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVP 159

Qy     116 APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
      ||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     160 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPAPAPAAPPSTPAAPKR 219

Qy     167 RG-SGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
      || ||||| ||||| ||||| ||||| ||||| |||||:|:| ||||| ||||| |||||
Db     220 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 278

Qy     226 LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285
      ||||| ||||| ||||| | :|||:| :||| |||:|:| :||| ||||| |||||
Db     279 LSPLSAAASFKEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 338

Qy     286 SEMGSSFKGSPKGESAILVENTKEEVI VRSKDKED-LVCSAALHSPQESPVG-----KED 339
      ||||| ||| |||:| | :|||:|:|:|:|:| | : ||: || | |||
Db     339 SEMGSSFSVSPKAESAVIVANPREEI IVKNDEEEKLVSNILHNNQQLPTALTCLKVKED 398

Qy     340 RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAWVEVKDITYEGSRDVLAA----RANV 395
      ||| || | ||| :|:| |||: ||||| |||||: |||||: | | |: ||| :|:
Db     399 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 457

Qy     396 ESKVDRKCLEDLSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
      |||||:| | ||||| : ||||| |:| ||||| :|| | ||||| | :|||
Db     458 ESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIA 517

Qy     455 ANTFPILLEDHTSENKTDEKKIEERKAQI I TEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
      | |||| | ||||| |||||: |||||: ||| || ||||| ||||| ||||| | :
Db     518 TNIFPLLGDPTSSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 577

Qy     514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573
      |||| |: ||||| ||||| ||||| ||||| |||||: ||||| : ||||| |||
Db     578 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTGIAYETKMDLVQTSEVMQESLYPAAQL 637

Qy     574 CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPEN 633
      |||||: ||||| ||||| ||||| : |||||: ||| ||||| |:|: ||| ||||

```

Db 638 CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPEN 696
 Qy 634 PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDF 692
 Db 697 PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDF 756
 Qy 693 SNYSEIAKFEKSVPEHAELVEDSSPESEPVDFSDDSIPEVPQTQEEAVMLMKESLTEVS 752
 Db 757 SDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLVKESLTETS 816
 Qy 753 -ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF 809
 Db 817 FESMIEYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEEL 876
 Qy 810 NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVS 868
 Db 877 STAVYSNDDLFISKEAQIRETETFSDSSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVS 936
 Qy 869 DKSEIANIQSGADSLPCLLEPCDLSPKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV 926
 Db 937 HKSEIANAPDGAGSLPCTELPHDL SLKNIQPKVEEKISFSDDFSNGSATS SKVLLLPDV 996
 Qy 927 SALEPQTEMGSIVKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986
 Db 997 SALATQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK 1056
 Qy 987 KTG VVFGAS-LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFR 1045
 Db 1057 KTG VVFGASAVFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFR 1116
 Qy 1046 AY---LESEVAISEELVQKYSNSALGHV-NSTIKELRR---LFLVDDLVD SLK-FAVLMW 1097
 Db 1117 AISGNLESCLYLRELGSGRYSNSALGSMWNCTVKGNFRAPSF FSWMDLVDSLRSFAVLMW 1176
 Qy 1098 VFTYVGALFNGLTLL-----ILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKI 1151
 Db 1177 VFTYVGCL--GLMVLDTTGFWALNFISSGSWLIYERHQAQIDHYLGLANKNVKDAMAKI 1234
 Qy 1152 QAKIPGLKRKAD 1163
 Db 1235 QAKIPGLKRKAE 1246

RESULT 14

AAAY71562

ID AAY71562 standard; Protein; 803 AA.

XX

AC AAY71562;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat Nogo A protein fragment used in the construction of mutant NiG.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.

XX

OS Rattus sp.

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US26160.

XX

PR 06-NOV-1998; 98US-0107446.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic
PT disorders of the central nervous system and inducing regeneration of
PT neurons -

XX

PS Example; Page -; 122pp; English.

XX

CC The patent relates to neurite growth inhibitor Nogo which is free of
CC all central nervous system (CNS) myelin material with which it is
CC natively associated. Nogo proteins and fragments displaying neurite
CC growth inhibitory activity are used in the treatment of neoplastic
CC disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,
CC craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic
CC neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma
CC and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
CC diseases. Therapeutics which promote Nogo activity can be used to treat
CC or prevent hyperproliferative or benign dysproliferative disorders e.g.
CC psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic
CC acids can be used to inhibit production of Nogo protein to induce
CC regeneration of neurons or to promote structural plasticity of the CNS
CC in disorders where neurite growth, regeneration or maintenance are
CC deficient or desired. The animal models can be used in diagnostic and
CC screening methods for predisposition to disorders and to screen for or
CC test molecules which can treat or prevent disorders or diseases of the
CC CNS. The present sequence is a fragment of rat Nogo A protein shown in
CC AAY71310, which is used in the construction of mutant NiG. The mutant
CC is composed of His-tag/T7-tag/Nogo-A sequence aa 172-974/His-tag.
CC Nogo A deletion mutants were used for mapping the inhibitory sites of
CC Nogo protein. Major inhibitory region was identified in the
CC Nogo A sequence from amino acids 172-974, particularly amino acids
CC 542-722. In addition, N-terminal region 1-171 was found to be inhibitory
CC to NIH 3T3 fibroblast spreading.

CC Note: The present sequence is not given in the specification but is
CC derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42
CC are referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However, the specification does not include sequences for
CC these SEQ ID numbers.

XX
SQ Sequence 803 AA;

Query Match 68.8%; Score 4023; DB 21; Length 803;
Best Local Similarity 99.9%; Pred. No. 1.1e-201;
Matches 802; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      172 VDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLST 231
      |||
Db      1 VDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLST 60

Qy     232 VSFKEHGYLGNL SAVSSSEGTIEETLINEASKELPERATNPFVNRDLAEFSELEYSEMGSS 291
      |||
Db     61 VSFKEHGYLGNL SAVSSSEGTIEETLINEASKELPERATNPFVNRDLAEFSELEYSEMGSS 120

Qy     292 FKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTM DIF 351
      |||
Db    121 FKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTM DIF 180

Qy     352 NEMQMSV VAPVREEYADFKPF EQAW EVKDTYEGSRDVL AARANVESKVDRCLEDSLEQK 411
      |||
Db    181 NEMQMSV VAPVREEYADFKPF EQAW EVKDTYEGSRDVL AARANVESKVDRCLEDSLEQK 240

Qy     412 SLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTD 471
      |||
Db    241 SLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTD 300

Qy     472 EKKIEERKAQII TEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDL 531
      |||
Db    301 EKKIEERKAQII TEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDL 360

Qy     532 VQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDI 591
      |||
Db    361 VQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDI 420

Qy     592 VMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEEAMNVALKALGTK 651
      |||
Db    421 VMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEEAMNVALKALGTK 480

Qy     652 EGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFS NYSEIAKFEKSVPEHAEL 711
      |||
Db    481 EGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFS NYSEIAKFEKSVPEHAEL 540

Qy     712 VEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESL TEVSETVAQHKEERLSASPQELG 771
      |||
Db    541 VEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESL TEVSETVAQHKEERLSASPQELG 600

Qy     772 KPYLESFQPNLHSTKDAASNDIPTLT KKEKISLQMEEFNTAIYSNDDLSSKEDKIKESE 831
      |||
Db    601 KPYLESFQPNLHSTKDAASNDIPTLT KKEKISLQMEEFNTAIYSNDDLSSKEDKIKESE 660

Qy     832 TFS DSSPIEI IDEFP T FVS AKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCD 891
      |||
Db    661 TFS DSSPIEI IDEFP T FVS AKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCD 720

Qy     892 LSFKN IY PKDEVHVSDEFSEN RSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKK 951
      |||
```

Db 721 LSFKNIPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKK 780

Qy 952 LPSDTEKEDRSLSAVLSAELSKT 974

Db 781 LPSDTEKEDRSLSAVLSAELSKT 803

RESULT 15

AA71386

ID AAY71386 standard; Protein; 737 AA.

XX

AC AAY71386;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat Nogo A protein fragment used in the construction of mutant NiG-D1.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; mutant; mutein.

XX

OS Rattus sp.

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US26160.

XX

PR 06-NOV-1998; 98US-0107446.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic
 PT disorders of the central nervous system and inducing regeneration of
 PT neurons -

XX

PS Example; Page -; 122pp; English.

XX

CC The patent relates to neurite growth inhibitor Nogo which is free of
 CC all central nervous system (CNS) myelin material with which it is
 CC natively associated. Nogo proteins and fragments displaying neurite
 CC growth inhibitory activity are used in the treatment of neoplastic
 CC disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,
 CC craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic
 CC neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma
 CC and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
 CC diseases. Therapeutics which promote Nogo activity can be used to treat

Db	421	VMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTK	480
Qy	652	EGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAEL	711
Db	481	EGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAEL	540
Qy	712	VEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELG	771
Db	541	VEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELG	600
Qy	772	KPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNNTAIYSNDDLSSKEDKIKESE	831
Db	601	KPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNNTAIYSNDDLSSKEDKIKESE	660
Qy	832	TFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCD	891
Db	661	TFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCD	720
Qy	892	LSFKNIYPKDEVHVSDE	908
Db	721	LSFKNIYPKDEVHVSDE	737

Search completed: December 19, 2003, 15:35:11
Job time : 52 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2003, 15:34:13 ; Search time 21 Seconds
(without alignments)
2343.216 Million cell updates/sec

Title: US-09-830-972-2
Perfect score: 5848
Sequence: 1 MEDIDQSSLVSSSTDSPRP.....VKDAMAKIQAKIPGLKRKAD 1163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	908	15.5	199	2	US-08-700-607-1
2	789.5	13.5	776	2	US-08-700-607-5
3	716.5	12.3	356	2	US-08-700-607-6
4	685	11.7	208	2	US-08-700-607-7
5	671	11.5	267	2	US-08-700-607-8
6	539.5	9.2	168	4	US-09-149-476-563
7	519	8.9	241	2	US-08-700-607-3
8	302.5	5.2	8991	4	US-08-714-741-32
9	286	4.9	92	4	US-09-149-476-411
10	279.5	4.8	1786	3	US-08-973-462-8
11	265.5	4.5	1780	1	US-08-769-309A-5

12	265.5	4.5	1780	3	US-08-994-570-5	Sequence 5, Appli
13	265	4.5	2137	4	US-09-134-001C-4463	Sequence 4463, Ap
14	254.5	4.4	1596	4	US-08-978-277A-4	Sequence 4, Appli
15	233	4.0	1142	2	US-08-993-118-7	Sequence 7, Appli
16	233	4.0	1142	3	US-08-845-528C-7	Sequence 7, Appli
17	233	4.0	1142	4	US-09-066-281B-7	Sequence 7, Appli
18	232.5	4.0	1805	1	US-07-853-913-2	Sequence 2, Appli
19	228	3.9	1142	3	US-09-061-709-2	Sequence 2, Appli
20	228	3.9	1142	4	US-09-899-651-2	Sequence 2, Appli
21	227	3.9	1270	4	US-07-757-022B-44	Sequence 44, Appl
22	227	3.9	1311	4	US-07-757-022B-42	Sequence 42, Appl
23	227	3.9	1313	4	US-07-757-022B-142	Sequence 142, App
24	227	3.9	1314	4	US-07-757-022B-50	Sequence 50, Appl
25	227	3.9	1320	4	US-07-757-022B-46	Sequence 46, Appl
26	227	3.9	1320	4	US-07-757-022B-60	Sequence 60, Appl
27	227	3.9	1354	4	US-07-757-022B-48	Sequence 48, Appl
28	227	3.9	1361	4	US-07-757-022B-40	Sequence 40, Appl
29	227	3.9	1363	4	US-07-757-022B-52	Sequence 52, Appl
30	227	3.9	1404	4	US-07-757-022B-2	Sequence 2, Appli
31	227	3.9	1404	4	US-07-757-022B-62	Sequence 62, Appl
32	225	3.8	688	3	US-09-141-047-8	Sequence 8, Appli
33	224.5	3.8	941	4	US-07-757-022B-14	Sequence 14, Appl
34	224.5	3.8	1022	4	US-07-757-022B-84	Sequence 84, Appl
35	224.5	3.8	1038	4	US-07-757-022B-74	Sequence 74, Appl
36	224.5	3.8	1049	4	US-07-757-022B-58	Sequence 58, Appl
37	224.5	3.8	1140	4	US-07-757-022B-104	Sequence 104, App
38	224.5	3.8	1346	2	US-08-635-121-2	Sequence 2, Appli
39	224.5	3.8	1346	4	US-08-978-277A-2	Sequence 2, Appli
40	224	3.8	630	3	US-08-973-462-9	Sequence 9, Appli
41	223	3.8	2409	6	5180808-2	Patent No. 5180808
42	222	3.8	1312	3	US-09-041-886-19	Sequence 19, Appl
43	222	3.8	1312	4	US-09-648-281-2	Sequence 2, Appli
44	220	3.8	1601	4	US-09-345-473E-40	Sequence 40, Appl
45	218.5	3.7	2842	1	US-07-741-940-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-08-700-607-1

; Sequence 1, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304


```

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5

```

```

Query Match          13.5%; Score 789.5; DB 2; Length 776;
Best Local Similarity 31.2%; Pred. No. 3.2e-42;
Matches 243; Conservative 115; Mismatches 252; Indels 169; Gaps 28;

```

```

QY      487 TSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGT 546
      : | : | ||: : : : : | : | || : | : | :
Db      65 SGPARGSP--VAMETASTGVAGVSSAMDHTFSTTSKDGE-----SCYTSLI-----S 110

QY      547 KIAETKVDLVQTSEAIQ-ESLYPTAQLCPSFEEAEATPSPVLPDI--VMEAPLNS----- 599
      | | : | : : | : : | | | ||| : : | |
Db      111 DICYPQEDSTYFTGILQKENGHVITISEP---EELGTPGPSLPDVPGIESRGLFSSDSG 167

QY      600 --LLPSAGASVVQPSVSPLEAPPPVSY-----DSIKLEPENPPPYEEA-----M 641
      : | : | : ||: : | : : | : : | : : | :
Db      168 IEMTPAESTEVNKKILADPLDQMKAEAYKYIDITRPEEVKHQEQHHPELEDKDLDFKNKDT 227

QY      642 NVALKALGTKEGIKEPE-----SFNAAVQETEAPYISACDLIKETKLSTE-PSP 690
      : : : | ||: ||: : : : : | ||| | | : | : : : |
Db      228 DISIK---PEGVREPDKPAPVEGKIIKDHLLEESTFAPYID---DLSEEQRRAPIITP 280

QY      691 DFSNYSEIAKFEKSVPEHAELVEDSSPESEPVDLF-SDDSIPEV----PQTQEEAVMLMK 745

```

```

      :||      |      ::|| : : | | :|| | :| :
Db      281 VKITLTEIE-----PSVETTTQEKTPKQDICKLKPSPDTVPTVTVSEPEDDSPGSITPP 334

Qy      746 ESLTEVSETVAQHK-----EERLSASPQELGKPYLESFQP-----NLHSTKDAASND----- 792
      ||| | :| | :|| : :| : | | : | : :
Db      335 SSGTEPSAAESQGKGSISEDELITAIKEAKGLSYETAENPRPVGQLADRPEVKARSGPPT 394

Qy      793 IPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKI----- 827
      ||: | | : : : | | : : || :
Db      395 IPSPLDHEASSAESGDSEIELVSEDPM--AAEDALPSGYVSFGHVGGPPPPSPASPSIQYS 452

Qy      828 ---KESETFSDSSPIEIIDFPTFVSAKDDSPKLAKEYTDLEVSDKSEI-----ANIQSG 879
      :| | || | :| | || :||| : : :| | :
Db      453 ILREEREAE LDS---ELIIESCDASSASEESPKREQDSPPMKPSALDAIREETGVRAEER 509

Qy      880 ADSLPCLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIV 939
      | | | | | : || : || | | | | | | | | | | |
Db      510 APSRRGLAEPG--SFLD-YPSTEPQPGPEL-----PPGDGALEPETPM----- 549

Qy      940 KSKSLTKEAEKKLPSDTEKEDRSLSAVLSAE-----LSKTSVVDLLYWRD 984
      || | :| : : : : | : | : |||||
Db      550 -----LPRKPEEDSSSNQSPAATKGPGLGPGAPPPLLFLNKQKAI D LLYWRD 597

Qy      985 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPF 1044
      ||: ||: ||: | | ||| ||: ||| ||: ||| || | ||||| | : ||: ||: |||||
Db      598 IKQTGIVFGSFLLLFLSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGHPF 657

Qy      1045 RAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGA 1104
      : |||| | : : || : |||| : ||||: ||||| ||||| ||||| ||||| : |||||
Db      658 KAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLMWLLTYVGA 717

Qy      1105 LFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRRAD 1163
      ||||| ||: ||: ||: ||: ||: || | ||| |||| : : ||||| || || :
Db      718 LFNGLTLLLMVAVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIPGAKRHAE 776

```

RESULT 3

US-08-700-607-6

; Sequence 6, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

Qy 1153 AKIPGLKRRKAD 1163
||||| || |:
Db 198 AKIPGAKRHAE 208

RESULT 5

US-08-700-607-8

; Sequence 8, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 281046

US-08-700-607-8

Query Match 11.5%; Score 671; DB 2; Length 267;
Best Local Similarity 66.3%; Pred. No. 2.4e-35;
Matches 124; Conservative 33; Mismatches 30; Indels 0; Gaps 0;

Qy 973 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1032
|: :|||||||:|:|:| | || ||| |:| | | ||||| |:
Db 9 KSQAIDLLYWRDIKQTGIVFGSFLLLLSLTQFSVSVVAYLALAALSATISFRIYKSVL 68

Qy 1033 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSKF 1092
 ||:||:||||||:|||| |: |:| :|||:: :|||:||||||| |||||
 Db 69 QAVQKTDEGHPFKAYLELEITLSQEQIQKYTDCLQLYVNSTLKELRRLFLVQDLVDLSKF 128
 Qy 1093 AVLMMWFTYVVGALFNGLTLLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQ 1152
 ||||: ||||| |||||::||:|:|:|:|:| :|| |:| |||| : :|||
 Db 129 AVLMWLLTYVVGALFNGLTLLMAVVSMTLPVVYVKHQAQVDQYLGLVRTHINTVVAKI 188
 Qy 1153 AKIPGLK 1159
 |||| :
 Db 189 AKIPGAR 195

RESULT 6

US-09-149-476-563

; Sequence 563, Application US/09149476
 ; Patent No. 6420526
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 186 Human Secreted proteins
 ; FILE REFERENCE: PZ002P1
 ; CURRENT APPLICATION NUMBER: US/09/149,476
 ; CURRENT FILING DATE: 1998-09-08
 ; EARLIER APPLICATION NUMBER: PCT/US98/04493
 ; EARLIER FILING DATE: 1998-03-06
 ; EARLIER APPLICATION NUMBER: 60/040,162
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,333
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/038,621
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,626
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,334
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,336
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,163
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/047,600
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,615
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,597
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,502
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,633
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,583
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,617
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,618
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,503

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594

```

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

```

```

Query Match          9.2%; Score 539.5; DB 4; Length 168;
Best Local Similarity 59.3%; Pred. No. 3.1e-27;
Matches 99; Conservative 36; Mismatches 31; Indels 1; Gaps 1;

```

```

Qy      998 LLLSLTVFSIVSVTAYIALLLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEE 1057
      :||| |::|| :|: ||||| |||||:|::|||:|:::| |
Db      1 MLLSLAAFVSVISVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSE 60

Qy     1058 LVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALI 1117
      | |:| :|: | :| : |||||:||||| || ||: |||||:|::||| | :
Db     61 AFHNYMNAAMVHINRALKLIIRLFLVEDLVDSLKLAVFMWLMITYVGAVFNGITLLILAE 120

```


Db 44 SSCAVHDLIXWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSV 103

Qy 1032 IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLK 1091
 |||:||||:||||:||||: :: :| | | |:|: |:| :| : |||||:|||||||

Db 104 IQAVQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHINRALKLIIRLFLVEDLVDSLK 163

Qy 1092 FAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQV 1131
 || ||: |||||:||||:||||| : : |:|:| :||:|

Db 164 LAVFMWLMTYVGAVFNGITLLILAELLIXSVPIVYXKYKV 203

RESULT 8

US-08-714-741-32

; Sequence 32, Application US/08714741

; Patent No. 6500613

; GENERAL INFORMATION:

; APPLICANT: Briles, David E.

; APPLICANT: McDaniel, Larry S.

; APPLICANT: Swiatlo, Edwin

; APPLICANT: Yother, Janet

; APPLICANT: Crain, Marilyn J.

; APPLICANT: Hollingshead, Susan

; APPLICANT: Tart, Rebecca

; APPLICANT: Brooks-Walter, Alexis

; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,

; TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,

; TITLE OF INVENTION: PORTIONS AND PRODUCTS

; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Curtis, Morris & Safford, P.C.

; STREET: 530 Fifth Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/714,741

; FILING DATE: 16-SEP-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Frommer Esq., William S.

; REGISTRATION NUMBER: 25,506

; REFERENCE/DOCKET NUMBER: 454312-2460

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 840-3333

; TELEFAX: (212) 840-0712

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8991 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: amino acid
US-08-714-741-32

Query Match 5.2%; Score 302.5; DB 4; Length 8991;
Best Local Similarity 22.1%; Pred. No. 1.4e-09;
Matches 244; Conservative 125; Mismatches 439; Indels 297; Gaps 47;

```
Qy      18 PRPPPAFKYQFVTEPEDEDEDEDEDEDEDEDEDEDELEEELEVLERKPAAGLSAAAVPPAAAAAP 77
      |:| || : :|| :||: ||| | || | :| || | |
Db      7805 PKPAPAPQPAPAPKPEKTDDQQAEEYARRSE--EEYNRLPQQQ-----PPKAEKP 7853

Qy      78 LLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLPPAAAVLPSKLPEDDEPP 137
      : | | | :|| | | |||| || | | | | | |
Db      7854 -----APAPKPEQPVPAEXPENP-----APAPK--PAXAPQPLKPEEPAEQP 7893

Qy     138 ARPPPPPPAGASPLAEPAPPSTPAAP--KRRGSGSVDETLFALPAASEPVISSAEKIM 195
      | ||| || | | || | : | :| | |
Db     7894 KPEKPEEPAGQ---PEPEKPDDQQAGEDYARRSGGEYNRFQQQPPKAEK--PAPAPK-- 7946

Qy     196 DLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSF-----KEHGYLGNLSAVSS 248
      ||| | ||: | :| | | | | | | | |
Db     7947 --PEQP-----VPAPKTLLKKAKLAGAKSKAATKKAEELEPELEKAEAELENLLSTLD 7996

Qy     249 SEGTIEETLNEASKELPERATNPFVNRDLAEFSEL--EYSEMGSFSGKSPKGESAILVEN 306
      || :| :| || | | : ||| | | : : | : :
Db     7997 PEG---KTQDELDKEAAEAELNKKVEALPNQVSELEEEELSKLEDNLKDAETNNVEDYIKE 8053

Qy     307 TKEEVIVRSK---DKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVAPVR 363
      || | : :| ||| : : | | | : || ||
Db     8054 GLEEAIATKQAELEKTPKELDAALN--ELGPDGDEEETPPPE-----APAE 8097

Qy     364 EEYADFKPFQAWEVKDTYEGSRDVLAAARANVESKVDRKCLED--SLEQKSLGKDSEGRN 421
      : : || : | | | | | : | : | | : | :
Db     8098 QPKPE-KPAETPAPAPKPEKSADQQA-----EEDYARRSEEEYNRLTQQQPPKAEKPAP 8151

Qy     422 EDASFPSTPEPVKDSSRAYITCASFTSA-----TESTTANTFPLLEDHT 465
      | | | | | || | | | | | | | | | |
Db     8152 APAPKPEQPAPA-PKSRGLATKKKLNLAEARIELLLKKLGLLEPGLEKAGAGLGNLLSTLD 8210

Qy     466 SENKTDE-----KKIEERKAQI--ITEKTSPKTSNPFLVAVQDSEADYVTTDT 511
      | || : ||: | : : | : | :| :| :|
Db     8211 PEGKTQDELDKEAAEAELNKKVEALPNQVAEELEELSKLEDN----LKDAETNHVEDYI 8265

Qy     512 LSKVTEAAVSNMPE-----GLTPDLVQE--ACESELNEATGTKIAYET--- 552
      : || : | || :| | | : : | | |
Db     8266 KEGLEEAIATKQAELEKTPKELDAALNELGPDGDEEETPAPEAPAEQPKPEKPAETPAP 8325

Qy     553 -----KVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAP---- 596
      : | : || | | | | | : | :| | |
Db     8326 APKPEKSADQQAEEYARRSEEEYNRL--TQQQPPKAEKPAPAPAP-KPEQPAPAPKKKQ 8382

Qy     597 -----LNSLLPSA-----GASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAM 641
      :|| | ||: : : | || :|| | | :
Db     8383 KVNLENLLSTLDPGGKTQDELDKGAAEAELNKKVEALPNPVX----ELEELSPPEDN-- 8436

Qy     642 NVALKALGT-----KEGIKE-----PESFNAAV-----QETEAPYIS 673
      || | |||:| | :||: :|| |
```

Db 8437 ---LKDAETNHVEDYIKEGLEEEAIATKQAELEETPQEVDAALNDLVPDGGEEETPAP--- 8490

Qy 674 IACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAE-----LVEDSSPESE 720
: : : |:|: : | ||| : || | : |:|

Db 8491 ----APQPDEPAPAPAPNAEQPAPAPKPEKSADQQAEDYARRSEGEYNRLTQQQPPKAE 8546

Qy 721 -PVDLFSDDSIPEVPQTQEEAVML-----MKESLTEVSETVAQHKEERLSASPQ 768
| : | :| | : : : | | :|: |:|

Db 8547 KPAPAPAPKPEQPAPAPNKEIARLQSDLKDAEENNVEDYIKEGLEQAITNKKAE LATTQQ 8606

Qy 769 ELGKPYLESFQPNLHSTKDAASNDIPTLTKE-----KISLQMEEFNTAIYSNDDLL 820
: | : | | |:| |:| : : :| : :|

Db 8607 NIDKTQKDLEDAELELEKVLATLDPEGKTQDELDKEAAEAELNEKVEALQNQVAELEEEEL 8666

Qy 821 SSKEDKIKESETFSDSSPI-EIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSG 879
| || :|:| | : | | :| : : :| | :|

Db 8667 SKLEDNLKDAETNNVEDYIKEGLEE-----AIATKKAELEKTQKE----- 8706

Qy 880 ADSLPCLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIV 939
| : : | : :| : | | | | :|

Db 8707 -----LDAALNELGPDGD---EETPAPAPQPEKPAEEPEN-PAPAPKPE----- 8747

Qy 940 KSKSLTKEAEKKLPSDTEKEDRSLS 964
|| :|:| : |:| | :

Db 8748 --KSADQQAEDYARRSEEEYNRLT 8770

RESULT 9

US-09-149-476-411

; Sequence 411, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZ002P1

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,334

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,163

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/047,600

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,615

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312

; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060

Query Match 4.9%; Score 286; DB 4; Length 92;
Best Local Similarity 56.0%; Pred. No. 2e-11;
Matches 51; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

```

QY      1064 NSALGHVNSTIKELRRLFLVDDLDVSLKFAVLMMWVFITYVGALFNGLTLLIILALISLFSIP 1123
      |:|: |:| :| :| ||||:||||| || ||: ||||:||||:||||| : :||:|
Db      2 NAAMVHINRALKLIIRLFLVEDLDVSLKLAVFMWLMITYVGAVFNGITLLILAELLIFSVP 61

QY      1124 VIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154
      ::||::: ||||:|:| | : || :|
Db      62 IVYEKYKTQIDHYVGIARDQTKSIVEKIPSK 92

```

US-08-973-462-8

Query Match 4.8%; Score 279.5; DB 3; Length 1786;
Best Local Similarity 20.1%; Pred. No. 3.9e-09;
Matches 261; Conservative 220; Mismatches 518; Indels 297; Gaps 60;

Qy	33	EDEEEEEEEEEDEEDEDLEEFLEVLERKPAAGLSAAAVPPAAAAPLLDFFSSDS----	VP	87
		: : : : : :		
Db	225	EKVEESVEENDEESVEENVEE-NVEENDDG--SVASSVEESIASSVDESIDSSI EENVA		280
Qy	88	P-----APRGPLPAAPPAAPERQPSWERSPA-----APAPSLPPAAAV-LPSKLPEDDE		135
		: : : : : : : :		
Db	281	PTVEEIVAPSVVESVAPSVEESVEENVEESVAENVEESVAENVEESVAENVEESVAENVE		340
Qy	136	PPARP-----PPPPPAGASPLAEPAAPSTPAAPKRRGSGSVDETLFALPAASEPVI PS		189
		: : : : :		
Db	341	EIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEESVEENVEESVAENV--EESVAENVEES		398
Qy	190	SAEKIMDLMEQPGNTVSSGOEDFPSVLLETAASL--PSLSPLSTVSFKEHGYLG NLSAVS		247

Db 399 VAENVEESVAE--NVEESVAENVEEIVAPTVEEIVAPTVEEIVAPSVVE-----SVAP 449
 Qy 248 SSEGTEETLNEASKELPERATNPFVNRLAEFSELEYSEMGSSFKGSPKGESAILVENT 307
 Db 450 SVEESVEENVEESVAENVEESVAENVEESVAENVE-----ES--VAENV 491
 Qy 308 KEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVPVREEYA 367
 Db 492 EESV---AENVEESVA----ENVEESVAENVEEIVAP--TVE-----EIVAPTVEEIV 535
 Qy 368 DFKPFEQ-AWEVKDTYEGSRDVLAAANVESKVDRKCLEDSELEQKSLGKDSEGRN-EDAS 425
 Db 536 APSVVESVAPSVEESVEENVEESVAE-NVEESVAEN-VEESVAENV--EESVAENVEEIV 591
 Qy 426 FPSTPEPVKDSSRAYITCASFTSATESTTANTFPILLEDHTSENKTDEKKIEERKAQIITE 485
 Db 592 APTVEEIVAPTVEEIVA----PSVVESVA----PSVEESVEEN-----VEESVAENVEE 637
 Qy 486 KTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQACESELNEATG 545
 Db 638 SVAENVEESVAENVEEIVAPTVEEIVAPTVEEIVAPSVVESVAPS-VEESVEENVEESVA 696
 Qy 546 TKIAYETKVDLVQTS--EAIQESLYPTAQ--LCPSFEEAEATPSPVLPDIMEAPLNSLL 601
 Db 697 ENVE-ESVAENVEESVAENVEESVAENVEEIVAPTVEEIVA--PTVEEIVAPSVVESVA 752
 Qy 602 PSAGASV-----VQPSVSPLEAPPPVSYDSIKLE 630
 Db 753 PSVEESVEENVEESVAENVEESVAENVEESVAENVEESVAPTVEEIVAP-----SVE 804
 Qy 631 PENPPPYEEAM-----NVALKALGTKEGIKEPESFNAAVQETEAPYISACDLIK 680
 Db 805 ESVAPSVEESVAENVATNLSNLLSLLGGIETEEIKDSILNEIEEVKENVVTILENVE 864
 Qy 681 ETKLSTEPSPDFSNYSEIAK-----FEKSVPEHAELV----EDSSPESEPVDLF-- 725
 Db 865 ET--TAESVTTFSNILEEIQENTITNDTIEEKLLELHENVLSAALENTQSEEEKKEVIDV 922
 Qy 726 -----SDDSIPEVPQTQEEAVMLMKESLTE-----VSETV 755
 Db 923 IEEVKEEVATTLIETVEQAEKSAANTITEIFENLEENAVESNENVAENLEKLNVTV 982
 Qy 756 AQHKEERLSASPQELGKPYLES--FQPNLHSTKDAASNDIPTLTK--KEKISLQMEE--- 808
 Db 983 LDKVEETVEISGESLENNEMDKAFFSEIFDNVKGIQENLLTGMFRSIETSIIVIQSEEKVD 1042
 Qy 809 FNTAIYSN--DDLSSKEDKIKESETFSDDSPI-EIIDEF-----PTFVS 850
 Db 1043 LNENVVSSILDNIENMKEGLLNKLENISSSTEGVQETVTEHVEQNVYVDVDVPAMKDQFLG 1102
 Qy 851 AKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPKDEVHVSDEFS 910
 Db 1103 ILNEAGGLKEMFFNLEDVFKSE-----SDVITVEEIKDEPVQKEV-EKETVSIIEEME 1154
 Qy 911 ENRSSV---SKASISPSNVSALEPQTEMGSIVKSKSLT-KEAEKKLPSDTEK-----EDR 961

Db 1155 ENIVDVLEEEKEDLTDKMIDAVEESI EISSDSKEETESIKDKEKDVSLVVEEVQDNDMDE 1214

Qy 962 SLSAVL-----SAELSKTSV-VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIA 1015
|: || || | :| :: : : |::| : : |: :

Db 1215 SVEKVLELKNMEEELMKDAVEINDITSKLI EETQELNEVEADLIKDME-----K 1263

Qy 1016 LALLSVTISFRIYKGVIA----IQK-SDEGHPPFRAYLESEVA---ISEELVQKYSN--S 1065
| | :| | :| | ::| :| | | : | : |: ::| |:

Db 1264 LKELEKALS-EDSKEIIDAKDDTLEKVI EEEHDITTTLDEVVELKDVEEDKIEKVSDLKD 1322

Qy 1066 ALGHVNSTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLTLLILALISLFSIPVI 1125
: :||:: | :::: | : : : :

Db 1323 LEEDILKEVKEIKE--LESEILEDYK-----ELKTIETDIL 1356

Qy 1126 YERHQVQIDHYLGLANKS--VKDAMAKIQAKIPGLK 1159
|: ::| |: : : || | | : : |:

Db 1357 EEKKEIEKDHFEKFEEEAEEIKDLEADILKEVSSLE 1392

RESULT 11

US-08-769-309A-5

; Sequence 5, Application US/08769309A

; Patent No. 5741890

; GENERAL INFORMATION:

; APPLICANT: Scott, John D.,

; APPLICANT: Nauert, Brian J.,

; APPLICANT: Klauck, Theresa M.

; TITLE OF INVENTION: Protein Binding Domains of Gravin

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower/233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/769,309A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5741890and, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 27866/33451

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-474-6300

; TELEFAX: 312-474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1780 amino acids

; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-769-309A-5

Query Match 4.5%; Score 265.5; DB 1; Length 1780;
Best Local Similarity 20.8%; Pred. No. 3e-08;
Matches 264; Conservative 146; Mismatches 486; Indels 371; Gaps 51;

```
Qy      11 SSSTDSPRRPPPA-----FKYQFVTE-----PEDE----EDEEEEEDEEED 47
      | | : | | | : | | : | | | | | : | : | : | : |
Db      277 SKSAESPTSPVTSETGSTFK-KFFTQGWAGWRKKTSTFRKPKEDEVEASEKKKEQEPEKVD 335

Qy      48 DEDLEELEVLERKPAAGLSAAAVPPAAAA--PLLDSSSDSVPPAPRGPLPAAPPAAPERQ 105
      | : : | | | | | | | | : | | | : | | |
Db      336 TEEDGKAEVASEKLTASEQAHPQEPASAEHPRLSAEYEKV-----ELPS-----EEQ 383

Qy     106 PSWERSPAAPAPSLPPAAAVLPSKLP-----EDDEPPARPPPPPPAGASP 150
      | : | : | : | | | | : | : | : | | : |
Db     384 VSGSQGPSEKPA-PLATEVFDEKIEVHQEEVVAEVHVSTVEERTEEQKTEVEETAGSVP 442

Qy     151 L-----AEP--AAPPSTPAAPKRRGSGSVDETLFALPAASEPVI PSSAEKIMDLMEQP 201
      | | | | | | | | | | | | | | : | : | : |
Db     443 AEELVGMDAEPQEAEPAKELVKLKETCVSGEDPTQGADLSPDEKVLSPPEGVVSEVEML 502

Qy     202 GNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLG-----NLSAVSSSEGTI 253
      : : | | | : | | | | : | | | : : | :
Db     503 SSQERMKVQGSPLKKLFTSTGLKKLS-----GKKQKGRGGGDEESGEHTQVPADSPDSQ 557

Qy     254 EETLNEASKELPERATN-PFVNRDLAEFSELEYSEMSSFKGSPKGESAILVENTKEEVI 312
      | | | : | | | : : | | : : | | | : | : |
Db     558 EEQKGESSASSPEEPEEITCLEKGLAEVQQDGEAEAGATSDGEKKREGVTPWASFKKMVT 617

Qy     313 VRSK-----DKE---DLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVAPV 362
      : : | | | | | | : : : : | : | |
Db     618 PKKRVRRPSESDKEDELDKVKSATLSSTEST-----ASEMQEEMKGSVEEPK 664

Qy     363 REEYADFKPFEQAWEV-----KDTYEGS 385
      | | : | | | | | : | | |
Db     665 PEEPKRKVDTSVSWEALICVGSSKKRARRRRSSSDEEGGPKAMGGDHQKADEAGKDKETGT 724

Qy     386 RDVLA-----ARANVESK-----VDRKCLEDSEQLKSLGKDS 417
      : | | | : | : | | : | : | : |
Db     725 DGILAGSQEHDPGQGSSEPEQAGSPTEGEGVSTWESFKRLVTPRKKSLSKLEKS--EDS 782

Qy     418 -EGRNEDASFPSTPEPVKDSS-----RAYITCASFTSATE--ST 453
      | : | | | | : | : | : | | |
Db     783 IAGSGVEHSTPDT-EPGKEESWVSIKKFI PGRKKRPDGKQEAPVEDAGPTGANEDDSD 841

Qy     454 TANTFPLLEDHTSENKTD-----KKIEERKAQIITEKTSPKTSNPFLVAVQD----- 501
      | | | | : | : | : | : | : | |
Db     842 VPAVVPLSEYDAVEREKMEAQQAQKGAEQPEQKAATEVSKELSESQVHMAAAVADGTRA 901

Qy     502 -----SEADYVTTDTLSK-----VTEAAVSNMPEG- 526
      : | | : | : | : | | : |
Db     902 ATIIERSPSWISASVTEPLEQVEAEALLTEEVLEREVIAEEEPPTVTEP----LPENR 957

Qy     527 -----LTPDLVQEA-CESELNEATGTGI-AYETKVDLVQTSEAIQESLYPTAQ 572
```

```

      |||: | | | ||: | | :| :| | :
Db      958 EARGDTVSEAEALTPEAVTAAETAGPLGSEEGTEASAAEETTEMVSAVSQLTDSPTDTEE 1017

Qy      573 L-----CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVS 623
      | | | | | : : | | | | : | |
Db      1018 ATPVQVEGGVPDIEEQERRTQEV LQAVAEKVKEESQLPGTG-----GPEDVLQP VQ 1069

Qy      624 YDSIKLEPENPPPYEEA-----MNVALK-----ALGTKEGIKEPESFNAAVQE 666
      : | | | | | : | | | | | | | | |
Db      1070 ----RAEAERPEEQAEASGLKKETDVVLKVDAQEA KTEPFTQGVVGTTPESFEKAPQV 1125

Qy      667 TEAPYISIACDLIKETKLSTEPSPD--FSNYSEIAKFEKSVPEHAELVEDSSPES--EPV 722
      ||: | : : | | : | : | : | | |
Db      1126 TES-----IESSELVTTCQAE TLAGVKSQEMVMEQAIP-----PDSVETPT 1166

Qy      723 DLFSDD SIP----EVPQTQEEAVMLMKESL TEVSETVAQH----KEERLSASPQELGKPY 774
      | : | | | : | | : | : | : | : | : |
Db      1167 DSETDGSTPVADFDAPGTTQ-----KDEIVEIHEENEVHLVPVRGTEAEAVPAQKERPP 1220

Qy      775 LESFQPNLHSTKDAASNDIPTLT KKEKISLQMEEFNTAIYSNDDLSSKEDIKESETF S 834
      | | | | | : | : | : | : | : | : |
Db      1221 APSSFVFQEETKE-----QSKMEDTLEHTDKEVSVETVSILSKTEGTQ EADQYA 1269

Qy      835 DSSPIEI-----IDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPC 885
      | : | | | | | | | | | : | : | | |
Db      1270 DEKTKDVPFFEGLEGSIDTGITVSREKVTEVALKGEGTEEA ECKKDDALELQSHAKSPPS 1329

Qy      886 LELPCDLSF-----KNIYPKDEVHVSDEFSEN RSS-----VSKASISPSNVSALEPQTE 934
      | : : | : | | : : | | : | : |
Db      1330 ---PVEREMVVQVEREKTEAEP THVNEEKLEHETAVTVSEEVSKQLLQTVNVP IIDGAKE 1386

Qy      935 MGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVF-- 992
      : | : | : : : : | : | : | : |
Db      1387 VSSLEGSPPPCLGQEEAVCTKI QVQSSEASFTLTAAAE EKV--LGETANI LETGETLEP 1444

Qy      993 -GASLFL 998
      | | | |
Db      1445 AGAHLVL 1451

```

RESULT 12

US-08-994-570-5

; Sequence 5, Application US/08994570

; Patent No. 6090929

; GENERAL INFORMATION:

; APPLICANT: Scott, John D.,

; APPLICANT: Nauert, Brian J.,

; APPLICANT: Klauck, Theresa M.

; TITLE OF INVENTION: Protein Binding Domains of Gravin

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower/233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,570
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090929and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33451
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1780 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-994-570-5

```

```

Query Match          4.5%; Score 265.5; DB 3; Length 1780;
Best Local Similarity 20.8%; Pred. No. 3e-08;
Matches 264; Conservative 146; Mismatches 486; Indels 371; Gaps 51;

```

```

Qy      11 SSSTDSPRPPPA-----FKYQFVTE-----PEDE----EDEEEEEDEEED 47
      | | :| | | : | | : | | | | | :| :| | | |
Db      277 SKSAESPTSPVTSETGSTFK-KFFTQGWAGWRKKTSTFRKPKEDEVEASEKKKEQEPEKVD 335

Qy      48 DEDLEELEVLERKPAAGLSAAAVPPAAAA--PLLDFFSSDSVPPAPRGPLPAAPPAAPERQ 105
      | : :| | | | | | | | :| | | : | | | | |
Db      336 TEEDGKAEVASEKLTASEQAHQPQEPASAEHPRLSAEYEKV-----ELPS-----EEQ 383

Qy      106 PSWERSPAAPAPSLPPAAAVLP SKLP-----EDDEPPARPPPPPPAGASP 150
      | : | : | : | | | | : | | | : | | | | |
Db      384 VSGSQGPSEKPA-PLATEVFDEKIEVHQEEVVAEVHVSTVEERTTEEQKTEVEETAGSVP 442

Qy      151 L-----AEP--AAPPSTPAAPKRRGSGSVDETFLFALPAASEPVI PSSAEKIMDLMEQP 201
      | | | | | | | | | | | | : | | | : | : |
Db      443 AEELVGMDAEPQEAEPAKELVKLKETCVSGEDPTQGADLSPDEKVL SKPPEGVVSEVEML 502

Qy      202 GNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLG-----NLSAVSSSEGTI 253
      : : | | | : | | | | : | | | : | : | :
Db      503 SSQERMKVQGSPLKKLFTSTGLKKLS-----GKKQKGRGGGDEESGEHTQVPADSPDSQ 557

Qy      254 EETLNEASKELPERATN-PFVNRDLAEFSELEYSEMGSSFKGSPKGESAILVENTKEEVI 312
      | | | :| | | | : : | | | : | | : | | | : | : |
Db      558 EEQKGESSASSPEEPPEITCLEKGLAEVQQDGEAEEGATSDGEKKREGVTPWASFKKMVT 617

Qy      313 VRSK-----DKE---DLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVAPV 362
      : : | | | | | | | | : : | | : | | | |
Db      618 PKKRVRRPSESDKEDEL DKVKSATLSSTEST-----ASEMQEEMKGSVEEPK 664

```

Qy 363 REEYADFKPFEQAWEV-----KDTYEGS 385
 || :|| || :|
 Db 665 PEEPKRKVDTSVSWEALICVGSSKKRARRRSSSDEEGGPKAMGGDHQKADEAGKDKETGT 724

 Qy 386 RDVLA-----ARANVESK-----VDRKCLEDSLEQKSLGKDS 417
 :|| | : | : || : ||: || :||
 Db 725 DGILAGSQEHDPGQSSSPEQAGSPTEGEGVSTWESFKRLVTPRKKS KSKLEEK--EDS 782

 Qy 418 -EGRNEDASFPSTPEPVKDSS-----RAYITCASFTSATE--ST 453
 | : | | | | | : | : | : | | | |
 Db 783 IAGSGVEHSTPDT-EPGKEESWVSIKKFI PGRKKRPDGKQEAPVEDAGPTGANEDDSD 841

 Qy 454 TANTFPLLEDHTSENKTDE-----KKIEERKAQII TEKTS PKTSNPFLVAVQD---- 501
 || | | : | : | : | : | : | : || |
 Db 842 VPAVVPLSEYDAVEREKMEAQQAQKGAEQPEQKAATEVSKELSESQVHMAAAVADGTRA 901

 Qy 502 -----SEADYVTTDTLSK-----VTEAAVSNMPEG- 526
 :|| :| : | : ||| :||
 Db 902 ATIIIEERSPSWISASVTEPLEQVEAEALLTEEVLEREVIAEEEEPPPTVTEP---LPENR 957

 Qy 527 -----LTPDLVQEA-CESELNEATGTKI-AYETKVDLVQTSEAIQESLYPTAQ 572
 |||: | | | | | | :| :| :| :| :| :|
 Db 958 EARGDTVVSEAELTPEAVTAAETAGPLGSEEGTEASAAEETTEMVSAVSQLTDSPDTTEE 1017

 Qy 573 L-----CPSFEEAEATPSPVLPDI VMEAPLNSLLPSAGASVVQPSVSPLEAPPPVS 623
 | || | || : : | || | : : ||
 Db 1018 ATPVQEVVEGGVPDIEEQERRTQEV LQAVAEKVKEESQLPGTG-----GPDVLPQPVQ 1069

 Qy 624 YDSIKLEPENPPPYEEA-----MNVALK-----ALGTKEGIKEPESFNAAVQE 666
 : | | | || : | || | | | ||| | |
 Db 1070 ----RAEAERPEEQAEASGLKKETDVVLKVDAQEA KTEPFTQGKVVGQTTPE SFEKAPQV 1125

 Qy 667 TEAPYISIACDLIKETKLSTEPSD--FSNYSEIAKFEKSVPEHAELVEDSSPES--EPV 722
 ||: | : : | | : | : | : | : | : |
 Db 1126 TES-----IESSELVTTCAETLAGVKSQEMVMEQAIP-----PDSVETPT 1166

 Qy 723 DLFSDDSIIP----EVPQTQEEAVMLMKESL TEVSETVAQH----KEERLSAS PQELGKPY 774
 | : | | : | | : | : | | : | : | : |
 Db 1167 DSETDGSTPVADFDAPGTTQ-----KDEIVEIHEENEVHLVPVRGTEAEAVPAQKERPP 1220

 Qy 775 LESFQPNLHSTKDAASNDIPTLT KKEKISLQMEEFN TAIYSNDDLSSKEDKIKESETFS 834
 | || : | : | : | : | : | : | : | :
 Db 1221 APSSSFVQEETKE-----QSKMEDTLEHTDKEVSVETVSILSKTEGTQEADQYA 1269

 Qy 835 DSSPIEI-----IDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPC 885
 | : : || | | | | : | : | : | | |
 Db 1270 DEKTKDVPPFEGLEGSIDTGITVSREKVTEVALKGEGTEEAECKDDALELQSHAKSPPS 1329

 Qy 886 LELPCDLSF-----KNIYPKDEVHVSDEFSENRSS-----VSKASISPSNVSALEPQTE 934
 | : : | : ||: | | : : ||| : || : : |
 Db 1330 ---PVEREMVVQVEREKTEAEPTHVNEEKLEHETAVTVSEEVSKQLLQTVNVPIIDGAKE 1386

 Qy 935 MGSIVKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVF-- 992
 : | : | : : : | : | : | : | : | : |
 Db 1387 VSSLEGSPPPCLGQEEAVCTKIQVQSSEASFTLTAAAEEEKV--LGETANI LETGETLEP 1444

 Qy 993 -GASLFL 998

Db 1445 AGAHLVL 1451

RESULT 13
US-09-134-001C-4463
; Sequence 4463, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4463
; LENGTH: 2137
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4463

Query Match 4.5%; Score 265; DB 4; Length 2137;
Best Local Similarity 19.6%; Pred. No. 4.3e-08;
Matches 172; Conservative 141; Mismatches 451; Indels 114; Gaps 24;

Qy 159 STPAAPKRRGSGSVDETLFALPAASEVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLE 218
|| : || : : : : : : : : : : : : : : : :
Db 990 STSTSTSDSASTSTSE-----SESDSASTSLSESTSTSVSDSTSTSTSDSASMSASESE 1043
Qy 219 TAASLPSLSPLSTVSFKEHGYLGNL SAV---SSSEGTIEETLNEASKELPERATNPVFN 275
: : ||| : : : : : : : : : : : : : : : :
Db 1044 SNSKSTSLSESTSTSLSE-----GSTSASTSDSASTSTSESESDSTSTSLSESTSTSLSGS 1098
Qy 276 DLAEFSELEYSEMGSSFKGSPKGESAILVE-----NTKEEVIVRSKDKEDLVC 323
| : : | : : || | : : : : : : : : : : : :
Db 1099 TSASTSD--SASTSTSESDSTSESTSLSESLSTSVSDSTASTSEASTSTSESESN 1155
Qy 324 SAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVAPVREEYADFKPFEQAWVKDTYE 383
| : | : : : : : : : : : : : : : : : :
Db 1156 STSLSGSLSTISDSTSTSTSDSASTSTSESESDSTSTSLSE-----STSTSLSDSTS 1208
Qy 384 GSRDVLAAARANVESKVDKCLEDSLEQK---SLGKDSEGRNEDASFPSTPEPVKDSSRAY 440
| : : || | : : | : : : : : : : : : : : :
Db 1209 TSTSESASTSTSES--DSTSESTSLSESTSTSVSDSTASTSDSASTSTSVSDSESASTS 1266
Qy 441 ITCASFTSATESTTANTFPLLEDHTSE--NKTDEKKIEERKAQIIITEKTS PKTSNPFLVA 498
| : : || : : || : : || : : : : : : : : : : : :
Db 1267 ISESLSTSVSDSTSTSTSDSASTSTSESDSTSESTSLSESI STSVSDSTASTSDSASTS 1326
Qy 499 VQDSEADYVTTD-----TL SKVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYE 551
: || : : : : : : : : : : : : : : : : : : : : : :

Db 1327 TSESESDSASTSLSGSTSTSLSDSTSTSTSDSASTSTSESDSERASTSLSGSTSTSLSDS 1386

Qy 552 TKV---DLVQTSEAIQESLYPTAQLCPSEAEATPSPVLPDIVMEAPLNSLLPSAGASV 608
| | | | : : | | : | | : : | | |

Db 1387 TSTSTSDSASTSTSVSDS-----NSASTSLSGSLSTSVSDSTSTSTSDSASAST 1435

Qy 609 VQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALK-ALGTKEGIKEPESFNAAVQET 667
| | | | : : : : : | : | | : : | :

Db 1436 ---SESDSERA-----STSLSGSTSTSI SDSTSTSTSDSASTSTSVSESNSTSTSTSES 1486

Qy 668 EAPYISIIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSD 727
: : | | | | : : : : : | | | : : | :

Db 1487 LSTSVS-----DSTSTSTSDSASTSTSVSDSDSASTSSSES SV--STSDSESTSTSTST 1536

Qy 728 DSI---PEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQE-----LGKPYLESFQ 779
| | | : : : | : | | : : : : | | | |

Db 1537 DSASTSTSVSESNSTSTSLSGSTSTSVSDSTSTSTSDSASASTSESDSDSASTSSSES SVS 1596

Qy 780 PNLH-----STKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFS 834
: : | | : : | : | : : : : : | | : |

Db 1597 TSVSDSTASTSESASTSTSVSDSNSASTSLSESTSTSLSDSTSMSTSDSASTSTSESDS 1656

Qy 835 DSSPIEIID-----EFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADS 882
| | : : | | | : : : : : | | : : : | | :

Db 1657 DSASTSLSDSTSTSVSESTSTSTSTSVSASNSTSTSLSDSRSTSLSDSTSTSTSESGSTS 1716

Qy 883 LPCLELPCDLSFKNIYPKDEVHVSDEFSEN--SSVSKASISPSNVSALEPQTEMGSIVK 940
| | : : : | | | : : | : : | : | | : : |

Db 1717 TS--ESDSDSASTSLSESTSTSI SDSTSTSTSDSASTSMSVSDSNRASTSLSDSTSTSVS 1774

Qy 941 SKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVD 978
: : | | | | | | : | | |

Db 1775 DSTSASTSESASTSTRESESTSASTSLS-ESTSTSVSD 1811

RESULT 14

US-08-978-277A-4

; Sequence 4, Application US/08978277A

; Patent No. 6582956

; GENERAL INFORMATION:

; APPLICANT: Gelman, Irwin H.

; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10112-0228

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/978,277A

Qy	287	EMGSSFKGSPK---GESAILVENTKE-----EVIVRSKDKEDLVCSAALHSPQESPVGKE	338
Db	682	ASSSDDEGGPRTLGGDSHRAEEASKDKEAGTDAVPASTQEQQDAQGSSSPFAGSPSEGE	741
Qy	339	-----DRVVSP-----EKTMDIFNEMQMSVVAPVREEYADFKPFQAW-EVKD	380
Db	742	GVSTWESFKRLVTPRKKSLSKLEEKAEADSSVEQLSTEIEPSREE-----SWVSIKK	792
Qy	381	TYEGSRDVLAAARANVESKVDRKCLEDSE-----LEQKSLGKDS	417
Db	793	FIPGRR-----KKRADGKQEQTAVEDSGPVEINEDDPNVPVAVPLSEYNAVEREKM--EA	845
Qy	418	EGRNE-----DASFPSTPEPVKDSSRAYITCASFTSAT	450
Db	846	QGNTQLPQLLGAVYVSEELSKTLVHTVSVVAIDGTRAVT--SVEERSPSWIS-ASVTEPL	902
Qy	451	ESTTANTFPLLEDHTSENKTDEKKIEERKAQIIITEKTSPTKSNPFLVAVQDSEADYVTTD	510
Db	903	EHTAGEAMPPVEEVT-----EKDIIAEETPVLTQ-TLPEG-----KDAHDDMTVSE	947
Qy	511	TLSKVTEAAVSNMPEGLTPDLVQEACES-ELNEATGTKIAYETKVDLVQTSEAIQESLYP	569
Db	948	-----VDFTSEAVTATETSEALRTEEVTEASGA---EETDMVSAVSQLTDSPDT	994
Qy	570	TAQLCP-----SFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPP	620
Db	995	TEEATPVQEVESGVLDTEEEERQTQAILQAVADKVKEESQVP-ATQTVQRTGSKALEKVE	1053
Qy	621	PVSYSYSIKLEPENPP-----PYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISI	674
Db	1054	EVEEDSEVLASEKEKDVMPKGPVQEAHAHL-AQGSETGQATPESLEVPEVTADVDHVA-	1111
Qy	675	ACDLIKETKLSTEP-SPDFSNYSEIAKFEKSVPEHAELVEDSSPESEFVDLFSDDS----	729
Db	1112	TCQVIKLQQLMEQAVAPESSETLTDSETNGSTPLADSDTADGTQQDETID--SQDSKATA	1169
Qy	730	-IPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQPNLHSTKDA	788
Db	1170	AVRQSQVTEEEAATAQKEEPTLNNVPAQEEH-----GEEPGRDVLEPTQQEL----TA	1220
Qy	789	ASNDIPTLTCK-----EKISLQMEEF-----NTAIYSNDDL----LS	821
Db	1221	AA--VPVLAKTEVGQEGEVDWLDGKVKKEQEVFVHSGPNSQKAADVTDSEVMGVAGCQ	1278
Qy	822	SKED-----KIKESETFSDSSPIEIIIDEFPTFVSAKDDSPKLAKEY-----TDL	865
Db	1279	EKESTEVQSLSLGEGEMETDVEK-EKRETKPEQVSEEGEQETAAPHEGTYGKPVLTLDL	1337
Qy	866	EVSDKSEIANIQSGADSLP-----CLE-----	887
Db	1338	PSSERKALGSLGGSPSLPDQDKAGCIEVQVQSLDTTVTQTAAEAVEKVIETVVISETGES	1397
Qy	888	-----LPCDLSFKNIYPKDEVHVSDEF---SENRSSVSKASISPSNVSALEPQTEMG	936
Db	1398	PECVGAHLLPAEKSSATGGHWTLOHAEDTVPLGPESOAESIPPIIVTPAPESTLHPDLO-G	1455

Db 13 SLLQSSSESPQSCP-----EGEDSQSPLQIQSSPESDDTLYPLQSPQSRSEG--- 60

Qy 67 AAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWE--RSPAAPAPSLPPAAA 124
: ||| : | | : | : : || : | |

Db 61 -----EDSSDPLQRPPEGKDSQSPLQIQSSPEGDDTQSPQLONSQSSPEG-- 105

Qy 125 VLPSKLPEDDEPPARPPPPPPAG---ASPLAEPAAP-----PSTPAAPKRRGSGS 171
: | | || | ||| ||: | : : |

Db 106 -----KDSLSPLEISQSPPEGEDVQSPLQNPASSFFSSALLSIFQSSPESIQSPFEG- 157

Qy 172 VDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFP-----SVLLE 218
| || :|: :: : : : | | || | ||

Db 158 -----FPQSVLQIPVSAASSSTLVSIFQSSPESTQSPFEGFPQSPLQIPVSRFSSTLLS 212

Qy 219 TAASLPSLSPLSTVSFKEHGYLGNL SAVSSSEG TIEETLNEASKELPERATNPFVNRDLA 278
| | | : : | : : ||| || : |||

Db 213 IFQSSPERSQRTSEGFAQSPLQIPVSSSSSS-----TLLSLFQSSPERTQ----- 257

Qy 279 EFSELEYSEMGSSEFKGSPKGESAILV----ENTKEEVIVRSKDKEDLVCSAALHSPQESP 334
| :|:| | : | : : | : : || : |

Db 258 -----STFEGFPQSPLQIPVSRFSSTLLSIFQSSPERTQSTFEGFAQSPLQIP 306

Qy 335 VGKEDRVV-----SPEKTMDIFNEMQMSVV-APVREEYAD--FKPFEQAWV-KDITYE 383
| |||:| | :|: | : : : | : | :|:|

Db 307 VSSSSSSTLLSLFQSSPERTQSTFEGFPQSLLQIPMTSSFSSTLLSIFQSSPESAQSTFE 366

Qy 384 GSRDVLAAARANVESKVDRKCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITC 443
| || :| : | | |

Db 367 G-----FPQSPLQIPGSPFSSTL 385

Qy 444 ASFTSATESTTANTF-----PLLEDHTSENKTDEKKIEERKAQIITEKTSPKTSNPFLV 497
| : : | :|| || || : | : :||:|

Db 386 LSLFQSSPERTHSTFEGFPQSPLQIPMTSSFSSTLLSILQ-----SSPESAQSAFE 436

Qy 498 AVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLV 557
| : : | : || | : : || | : : | : |

Db 437 GFPQSPLQIPVSSSFSYTLLSLFQSSPE-RTQSTFEGFPQSPLQIPVSSSSSSSTLLSLF 495

Qy 558 QTSEAIQESLY-----PTAQLCPSEEEAATPSPVLPDIVMEAP--LNSL-----LPS 603
| :| : : | : | | | ||| : || | :|| |

Db 496 QSSPECTQSTFEGFPQSPLQIQSPPEGENTHSPL--QIVPSLPEWEDSLSPHYFPQSPP 553

Qy 604 AGASVVQPSVSPLEAPP-----PVSYDSIKLE--PENPPPYEEAMNVALKA 647
| : | | :|| | || : | :|| | :|:|

Db 554 QGEDSLSPHYFP-QSPPOGEDSLSPHYFPQSPQGEDSLSPHYFPQSPPOGEDSMSPLYFP 612

Qy 648 LGTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPE 707
: | | | : :| :|| | | : || : : | : :

Db 613 QSPLQG---EEFQSSLQSP---VSI-CS-----SSTPSSLPQSFPESSQSPPEGPV 656

Qy 708 HAELVEDSSPESEPVDFSD-----DSIPE-----VPQTQEEAVMLMKESLTEVS 752
: | ||:| | : | :|| | :||: | :||:|

Db 657 QSPL--HSPQSPPEGMHSQSPLQSPESAPEGEDSLSPQLQIPQSPLEG---EDSLSSLH 709

Qy 753 ETVAQHKEERLSASPQELGK--PYLESFQPNLHS----TKDAASNDIPTLTKEKIS--- 803
: : | | || : | | || :| | : | : |

Db 710 FPQSPPEWED-SLSPHLFPQFPQGEDFQSSLQSPVSI CSSSTSLSLPQSFPESPQSPPE 768

Qy 804 -----LQMEEFNNTAIYSNDDLSSKEDIKESETFSDSSPIEI-IDEFPTFVSAKDDSP 856
 Db 769 GPAQSPLQRPVSSFFSYTLASLLQSSHESQPSPPEGPAQSPLQSPVSSFPSSTSS----- 823

Qy 857 KLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPKDEVH---VSDEFSEN 913
 Db 824 -----SLSQSSPVSSFPSSTSS-----SLSKSSPESPLQSPVISFSSSTSL 864

Qy 914 SSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSD-----TEKEDR----- 961
 Db 865 SPFSEESSPVVD---EYTSSSDTLLESDSLT-DSESLIESEPLFTYTLDEKVDELARFL 919

Qy 962 -----SLSAVLSAELSK-TSVVDLLYWRDIKKTGVVFGASL 996
 Db 920 LLKYQVKQPITKAEMLTNVISRYTGYFPVIFRKAREFIEILFGISL 965

Search completed: December 19, 2003, 15:37:55
 Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2003, 15:36:49 ; Search time 40 Seconds
(without alignments)
5430.007 Million cell updates/sec

Title: US-09-830-972-2
Perfect score: 5848
Sequence: 1 MEDIDQSSLVSSSTDSPRP.....VKDAMAKIQAKIPGLKRRKAD 1163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

1	5848	100.0	1163	9	US-09-893-348-18	Sequence 18, Appl
2	4403.5	75.3	1192	9	US-09-758-140-6	Sequence 6, Appli
3	4403.5	75.3	1192	9	US-09-972-599A-6	Sequence 6, Appli
4	4403.5	75.3	1192	15	US-10-060-036-71	Sequence 71, Appl
5	4398.5	75.2	1192	9	US-09-789-386-2	Sequence 2, Appli
6	4398.5	75.2	1192	9	US-09-893-348-23	Sequence 23, Appl
7	1513	25.9	379	12	US-10-205-194-164	Sequence 164, App
8	1411.5	24.1	360	9	US-09-893-348-20	Sequence 20, Appl
9	1191	20.4	373	9	US-09-789-386-6	Sequence 6, Appli
10	1191	20.4	373	9	US-09-765-205-6	Sequence 6, Appli
11	1191	20.4	373	9	US-09-893-348-24	Sequence 24, Appl
12	1191	20.4	373	15	US-10-060-036-72	Sequence 72, Appl
13	925	15.8	199	9	US-09-893-348-21	Sequence 21, Appl
14	908	15.5	199	9	US-09-893-348-25	Sequence 25, Appl
15	888	15.2	289	9	US-09-789-386-4	Sequence 4, Appli
16	801	13.7	777	12	US-10-205-219-93	Sequence 93, Appl
17	671	11.5	267	12	US-10-205-194-127	Sequence 127, App
18	625.5	10.7	236	9	US-09-729-674-20	Sequence 20, Appl
19	625.5	10.7	236	9	US-09-765-205-26	Sequence 26, Appl
20	625.5	10.7	269	15	US-10-106-698-6222	Sequence 6222, Ap
21	539.5	9.2	168	11	US-09-809-391-563	Sequence 563, App
22	539.5	9.2	168	12	US-09-882-171-563	Sequence 563, App
23	345.5	5.9	1095	15	US-10-128-714-8305	Sequence 8305, Ap
24	341	5.8	1000	15	US-10-128-714-3305	Sequence 3305, Ap
25	321	5.5	66	9	US-09-758-140-20	Sequence 20, Appl
26	321	5.5	66	9	US-09-972-599A-20	Sequence 20, Appl
27	320	5.5	66	9	US-09-972-599A-22	Sequence 22, Appl
28	320	5.5	66	11	US-09-972-546-7	Sequence 7, Appli
29	309.5	5.3	98	15	US-10-050-704-179	Sequence 179, App
30	286	4.9	92	11	US-09-809-391-411	Sequence 411, App
31	286	4.9	92	12	US-09-882-171-411	Sequence 411, App
32	284.5	4.9	161	9	US-09-925-302-808	Sequence 808, App
33	279.5	4.8	1786	10	US-09-742-096-3	Sequence 3, Appli
34	272.5	4.7	2665	9	US-09-864-761-34248	Sequence 34248, A
35	272.5	4.7	3664	15	US-10-177-293-423	Sequence 423, App
36	271.5	4.6	2701	15	US-10-171-311-83	Sequence 83, Appl
37	267	4.6	1781	9	US-09-738-877-3	Sequence 3, Appli
38	267	4.6	1781	11	US-09-961-403-13	Sequence 13, Appl
39	260	4.4	1325	9	US-09-864-761-35612	Sequence 35612, A
40	259.5	4.4	617	9	US-09-864-761-36182	Sequence 36182, A
41	259.5	4.4	617	12	US-10-029-386-32114	Sequence 32114, A
42	255.5	4.4	1178	15	US-10-128-714-8240	Sequence 8240, Ap
43	255	4.4	5877	15	US-10-142-515-11	Sequence 11, Appl
44	255	4.4	5935	15	US-10-243-243A-8	Sequence 8, Appli
45	254.5	4.4	1596	10	US-09-902-432-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-893-348-18

; Sequence 18, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

```

; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-18

```

```

Query Match          100.0%; Score 5848; DB 9; Length 1163;
Best Local Similarity 100.0%; Pred. No. 5.7e-287;
Matches 1163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEELEVLERK 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEELEVLERK 60

Qy     61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120

Qy    121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAAPPSTPAAPKRRGSGSVDETFLFALP 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAAPPSTPAAPKRRGSGSVDETFLFALP 180

Qy    181 AASEVPVPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AASEVPVPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240

Qy    241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSEFKGSPKGES 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSEFKGSPKGES 300

Qy    301 AILVENTKEEVI VRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AILVENTKEEVI VRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA 360

Qy    361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLEDSEGR 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLEDSEGR 420

```

Qy	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA	480
Db	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA	480
Qy	481	QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Db	481	QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Qy	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Db	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Qy	601	LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEAMNVALKALGTKEGIKEPESF	660
Db	601	LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEAMNVALKALGTKEGIKEPESF	660
Qy	661	NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Db	661	NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Qy	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Db	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Qy	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Db	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Qy	841	IIDEFPFTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Db	841	IIDEFPFTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Qy	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED	960
Db	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED	960
Qy	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Db	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Qy	1021	VTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Db	1021	VTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Qy	1081	FLVDDLVDLKFVFLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA	1140
Db	1081	FLVDDLVDLKFVFLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA	1140
Qy	1141	NKSVKDAMAKIQAKIPGLKRRKAD	1163
Db	1141	NKSVKDAMAKIQAKIPGLKRRKAD	1163

RESULT 2

US-09-758-140-6

; Sequence 6, Application US/09758140

; Patent No. US20020012965A1

```
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of
Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-140-6
```

```
Query Match          75.3%; Score 4403.5; DB 9; Length 1192;
Best Local Similarity 75.9%; Pred. No. 4.7e-214;
Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;
```

```
Qy      1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
      |||:|||| ||||| ||||| ||||| ||||| |||||:|::| ||||| |||||
Db      1 MEDLDQSPLVSSS-DSPRRQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEEVLERK 58

Qy     61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
      ||||| || || |||:| | :| ||||| ||||| ||||| |||||: || : |
Db     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVP 118

Qy    116 APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
      ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178

Qy    167 RG-SGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
      || ||||| ||||| ||||| ||||| ||||| |||||:|: ||||| |||||
Db    179 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237

Qy    226 LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285
      ||||| ||||| ||||| | :|||:| :|||:| :| :||| |||||
Db    238 LSPLSAAAFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297

Qy    286 SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339
      ||||| || |||:| | :|:|:|:|:|:| | : ||: || | |||
Db    298 SEMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKED 357

Qy    340 RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAWVEVKDITYEGSRDVLAA----RANV 395
      ||| || | ||| :|| ||:|||||||: ||||: | | |:| | :|
Db    358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy    396 ESKVDRKCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSRAYITCASFT-SATESTT 454
      ||||:| || ||| : ||| |:| ||||| :|| | ||||| | :|||
Db    417 ESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIA 476
```



```

; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-599A-6

```

```

Query Match          75.3%; Score 4403.5; DB 9; Length 1192;
Best Local Similarity 75.9%; Pred. No. 4.7e-214;
Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;

```

```

Qy      1 MEDIDQSSLVSSSTDSPRRPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
      |||:|||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MEDLDQSPLVSSS-DSPRRQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEEVLERK 58

Qy     61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
      ||||| || || ||| |||:| | :| ||||| ||||| ||||| |||||: || : |
Db     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVP 118

Qy    116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
      ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178

Qy    167 RG-SGSVDETLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    179 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237

Qy    226 LSPLSTVSFKEHGYLGNLSAVSSSEGTIETLNEASKELPERATNPVNRDLAEFSELEY 285
      ||||| ||||| ||||| | :|||:| :|||:| :| :||| |||||
Db    238 LSPLSAAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297

Qy    286 SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339
      ||||| || ||| |||:| | :||:| ||:|:|:|:| || : ||: || | |||
Db    298 SEMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKED 357

Qy    340 RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANV 395
      ||| || | ||| :||:| ||:||||||| |||||: |||||: || ||: ||| :|:
Db    358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy    396 ESKVDRKCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
      |||||:| ||||| : |||| | :| ||||| :|| | ||||| | :|||
Db    417 ESKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIA 476

Qy    455 ANTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513

```

Db	477	TNIFPLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVLVAAQDSETDYVTTDNLT	536
Qy	514	KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL	573
Db	537	KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL	596
Qy	574	CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPEN	633
Db	597	CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPS SSPLEA-SSVNYESIKHEPEN	655
Qy	634	PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDF	692
Db	656	PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDF	715
Qy	693	SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS	752
Db	716	SDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETS	775
Qy	753	-ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF	809
Db	776	FESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEEL	835
Qy	810	NTAIYSNDDLLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVS	868
Db	836	STAVYSNDDLFISKEAQIRETETFSDDSPPIEIIDEFPTLISSKTD SFSKLAREYTDLEVS	895
Qy	869	DKSEIANIQSGADSLPCLLELPDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV	926
Db	896	HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDPV	955
Qy	927	SALEPQTEMGSIVKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK	986
Db	956	SALATQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK	1015
Qy	987	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1046
Db	1016	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1075
Qy	1047	YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALF	1106
Db	1076	YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALF	1135
Qy	1107	NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD	1163
Db	1136	NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 4

US-10-060-036-71

; Sequence 71, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Persing, David H.

```
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-71
```

```
Query Match          75.3%; Score 4403.5; DB 15; Length 1192;
Best Local Similarity 75.9%; Pred. No. 4.7e-214;
Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;
```

```
Qy      1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
      |||:|||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      1 MEDLDQSPLVSSS-DSPPRQPAPFKYQFVREPEDEE-EEEEEEEEDEDEDLEEEVLERK 58

Qy     61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
      ||||| || ||| |||:| | :| ||||| ||||| ||||| |||:| | :| |
Db     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDFSPVSSTVP 118

Qy    116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
      ||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPPSTPAAPKR 178

Qy    167 RG-SGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    179 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237

Qy    226 LSPLSTVSFKEHGYLGNLSAVSSSEGTIETLNEASKELPERATNPFVNRDLAEFSELEY 285
      ||||| ||||| ||||| | :|||:| :|||:| :| :| :||| |||||
Db    238 LSPLSAAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297

Qy    286 SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339
      ||||| || ||| |||:| | :|||:| :|||:| :| :| :||| |||||
Db    298 SEMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNNQQLPTALTCLVKED 357

Qy    340 RVVSPEKTMDFNEMQMSVVPVREEYADFKPFQAWEVKDTYEGSRDVLAA----RANV 395
      ||| || | ||| :|:| ||:||||||| |||:| |||:| | :||| :|:
Db    358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy    396 ESKVDRKCLEDLSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
      |||||:| ||||| : ||||| |:| ||||| :||| ||||| | :|||
Db    417 ESKVDKKCFADSLEQTNHEKDESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIA 476

Qy    455 ANTFPILLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
      | |||| | ||||| |||||:||||:||| || ||||| ||||| ||||| | :
Db    477 TNIFPLLGDPTSENKTDEKKIEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 536

Qy    514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573
      |||| |:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```



```
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-2
```

```
Query Match          75.2%; Score 4398.5; DB 9; Length 1192;
Best Local Similarity 75.9%; Pred. No. 8.4e-214;
Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;
```

```
Qy      1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
      |||:|||| |||| |||| |||| |||| |||| ||||:|:|:|||||||
Db      1 MEDLDQSPLVSSS-DSPRRQPAPFKYQFVREPEDEE-EEEEEEDEDEDLEEEVLERK 58

Qy     61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
      ||||| || || |||:| | :| ||||| ||||| ||||| ||| : |
Db     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVP 118

Qy    116 APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
      ||| |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPPSTPAAPKR 178

Qy    167 RG-SGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
      || ||||| ||||| ||||| ||||| ||||| |||||:|:| ||||| |||||
Db    179 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237

Qy    226 LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285
      ||||| ||||| ||||| | :|||:| :|||:|:|:| |||||:|:| :||| |||||
Db    238 LSPLSAAASFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297

Qy    286 SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339
      ||||| || || |||:| | :|||:|:|:|:|:| ||| : ||| |||
Db    298 SEMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQOELPTALTKLVKED 357

Qy    340 RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAWEVKDTYEGSRDVLAA----RANV 395
      ||| || | ||| :||| ||:||||||| |||||:| |||:| ||| :|:
Db    358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy    396 ESKVDRKCLEDSELEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
      |||||:| ||||| : ||||| |:| ||||| :|| ||||| | :|||
Db    417 ESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRPGAYITCAPFNPAAATESIA 476

Qy    455 ANTFPILLEDHTSENKTDEKKIEERKAQIIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
      | |||| | ||||| |||||:| |||:| ||| ||||| ||||| ||||| | :
Db    477 TNIFPLLGDPTSSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 536

Qy    514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTGKIAYETKVDLVQTSEAIQESLYPTAQL 573
      |||| | :||| ||||| ||||| ||||| |||||:| ||||| :||| |||
Db    537 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTGKIAYETKMDLVQTSEVMQESLYPAAQL 596

Qy    574 CPSFEEAEATPSPVLPDIMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPEN 633
      |||||:| ||||| ||||| ||||| :||| |||||:| ||| ||||| |:|:| |||
```

Db 597 CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPEN 655

Qy 634 PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDF 692
 |||||:|:| : | || ||||: ||:||||||| ||:|

Db 656 PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDF 715

Qy 693 SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS 752
 |:|:|:| | : |:|:|:|||||:|||||||:| | |:| |:|:|

Db 716 SDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS 775

Qy 753 -ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF 809
 |: : : : |:| | | |||||: : | :| : : |:|:| | |

Db 776 FESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLOMEEL 835

Qy 810 NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIDFPTFVSAKDDS-PKLAKEYTDLEVS 868
 :|:|:| | | : |:|:|:|||||:|||||:| | |:|:|

Db 836 STAVYSNDDLFIKSEAQIRETETFSDSSPIEIIDFPTLISSKTDSFSKLAREYTDLEVS 895

Qy 869 DKSEIANIQSGADSLPCLLPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV 926
 ||||| | ||| ||| ||| ||| || : : |:|:| | : | : |

Db 896 HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSKVLLLPDV 955

Qy 927 SALEPQTEMGSIIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986
 ||| | : | | | | | ||||| ||: | |||||

Db 956 SALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK 1015

Qy 987 KTG VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRA 1046
 |||||

Db 1016 KTG VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRA 1075

Qy 1047 YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF 1106
 |||||

Db 1076 YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF 1135

Qy 1107 NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRRAD 1163
 |||||:|:|:| |||||:|:|:|

Db 1136 NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRRAE 1192

RESULT 6

US-09-893-348-23

; Sequence 23, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

```

; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-23

```

```

Query Match          75.2%; Score 4398.5; DB 9; Length 1192;
Best Local Similarity 75.9%; Pred. No. 8.4e-214;
Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;

```

```

Qy      1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
      |||:|||| |||| |||| |||| |||| ||||:||||:|||||||
Db      1 MEDLDQSPLVSSS-DSPPRQPAPFKYQFVREPEDEE-EEEEEEEEDEDEDLEEEVLERK 58

Qy     61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
      ||||| || ||| |||:| | :| ||||| ||||| |||||:| | : |
Db     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSTVP 118

Qy    116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
      ||| ||| ||||| ||||| ||||| || || ||||| |||||
Db    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKR 178

Qy    167 RG-SGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
      || ||||| ||||| ||||| |||| ||| |||||:|:| ||||| |||||
Db    179 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237

Qy    226 LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285
      |||| |||| ||||| | :|||:| :|||:| :| :||| |||||
Db    238 LSPLSAAAFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297

Qy    286 SEMGSSFKGSPKGESAILVENTKKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339
      ||||| ||| |||:| | :||:|:|:|:|:| | : ||: || | |||
Db    298 SEMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLVKED 357

Qy    340 RVVSPEKTMDIFNEMQMSVVAPVREEYADFKPFQAWVEVKDTEYEGSRDVLAA----RANV 395
      ||| || | ||| :||| ||:|||||||:| ||||:| | |:||| :|:
Db    358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy    396 ESKVDRKCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
      ||||:| |||| : |||| |:| ||||| :|| ||||| | :|||
Db    417 ESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIA 476

Qy    455 ANTFPILLEDHTSENKTDEKKIEERKAQIIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
      | |||| | ||||| |||||:||||:|| || ||||| |||| ||||| :|
Db    477 TNIFPLLGDPTSENKTDEKKIEEKKAIIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 536

Qy    514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTGKIAYETKVDLVQTSEAIQESLYPTAQL 573
      |||| |:||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    537 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTGKIAYETKMDLVQTSEVMQESLYPAAQL 596

```



```
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Foocen-m2 reticulon
US-10-205-194-164
```

```
Query Match          25.9%; Score 1513; DB 12; Length 379;
Best Local Similarity 32.6%; Pred. No. 8.1e-69;
Matches 379; Conservative 0; Mismatches 0; Indels 784; Gaps 1;
```

```
Qy      1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60

Qy     61 PAAGLSAAAVPPAAAAPLLDfSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 PAAGLSAAAVPPAAAAPLLDfSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120

Qy    121 PAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSVDETLFALP 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 PAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSVDETLFALP 180

Qy    181 AASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240
      |||||||||
Db    181 AASEPVI PSSA----- 191

Qy    241 GNLSAVSSSEGtIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSsFKGSPKGES 300
Db    192 ----- 191

Qy    301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMdIFNEMQMSVVA 360
Db    192 ----- 191

Qy    361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLEDsLEQKSLGKDSEGR 420
Db    192 ----- 191

Qy    421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA 480
Db    192 ----- 191

Qy    481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540
Db    192 ----- 191

Qy    541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNsl 600
Db    192 ----- 191

Qy    601 LPSAGASVVQPSVSPLEAPPPVSyDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF 660
Db    192 ----- 191
```

Qy 661 NAAVQETEAPYISACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720

Db 192 ----- 191

Qy 721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQP 780

Db 192 ----- 191

Qy 781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE 840

Db 192 ----- 191

Qy 841 IIDEFPPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900

Db 192 ----- 191

Qy 901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED 960

Db 192 ----- 191

Qy 961 RLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 1020

Db 192 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 236

Qy 1021 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080

Db 237 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 296

Qy 1081 FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 1140

Db 297 FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 356

Qy 1141 NKSVKDAMAKIQAKIPGLKRKAD 1163

Db 357 NKSVKDAMAKIQAKIPGLKRKAD 379

RESULT 8

US-09-893-348-20

; Sequence 20, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

```
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-893-348-20
```

Qy	1	MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEELEVLERK	60
Db	1	MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEELEVLERK	60
Qy	61	PAAGLSAAAVPPAAAAPLLDFFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP	120
Db	61	PAAGLSAAAVPPAAAAPLLDFFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP	120
Qy	121	PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPSTPAAPKRRGSGSVDETLFALP	180
Db	121	PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPSTPAAPKRRGSGSV-----	172
Qy	181	AASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL	240
Db	173	-----	172
Qy	241	GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSFPGSPKGES	300
Db	173	-----	172
Qy	301	AILVENTKEEVIVRSKDKEDLVCSAALHSPQESVPGKEDRVVSPEKTMDIFNEMQMSVVA	360
Db	173	-----	172
Qy	361	PVREEYADFKPFQAWVEVKDITYEGSRDVLAAARANVESKVDKCLEDSLEQKSLGKDSEGR	420
Db	173	-----	172
Qy	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPILLEDHTSENKTDEKKIEERKA	480
Db	173	-----	172
Qy	481	QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Db	173	-----	172
Qy	541	NEATGTKIAYETKVLDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Db	173	-----	172
Qy	601	LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660

Db 173 ----- 172
 Qy 661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720
 Db 173 ----- 172
 Qy 721 PVDLFSDDSIPEVPQTQEEAVMLKESLTVSETVAQHKEERLSASPQELGKPYLESFQP 780
 Db 173 ----- 172
 Qy 781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE 840
 Db 173 ----- 172
 Qy 841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900
 Db 173 ----- 172
 Qy 901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED 960
 Db 173 ----- 172
 Qy 961 RLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 1020
 Db 173 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 217
 Qy 1021 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080
 Db 218 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 277
 Qy 1081 FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 1140
 Db 278 FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 337
 Qy 1141 NKSVDAMAKIQAKIPGLKRRAD 1163
 Db 338 NKSVDAMAKIQAKIPGLKRRAD 360

RESULT 9

US-09-789-386-6

; Sequence 6, Application US/09789386
 ; Patent No. US20020010324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MICHALOVICH, DAVID
 ; APPLICANT: PRINJHA, RABINDER KUMAR
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; FILE REFERENCE: GP-30165-C1
 ; CURRENT APPLICATION NUMBER: US/09/789,386
 ; CURRENT FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: U.K. 9916898.1
 ; PRIOR FILING DATE: 1999-07-19
 ; PRIOR APPLICATION NUMBER: U.K. 9816024.5
 ; PRIOR FILING DATE: 1998-07-22
 ; PRIOR APPLICATION NUMBER: US 09/359,208
 ; PRIOR FILING DATE: 1999-07-22

```
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-6
```

```
Query Match          20.4%; Score 1191; DB 9; Length 373;
Best Local Similarity 27.8%; Pred. No. 1.4e-52;
Matches 327; Conservative 12; Mismatches 20; Indels 818; Gaps 7;
```

```
Qy      1 MEDIDQSSLVSSSTDSPRPPPAFKYQFVTEPEDEDEEEEEDEEDEDLEEEVLERK 60
      |||:|||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MEDLDQSPLVSSS-DSPRPPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEEVLERK 58

Qy     61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
      ||||| || ||| |||:| | :| ||||| ||||| ||||| ||||| |||||
Db     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSSTVP 118

Qy    116 APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
      ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPPSTPAAPKR 178

Qy    167 RGSGSVDETLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL 226
      |||
Db    179 RGSS----- 182

Qy    227 SPLSTVSFKEHGYLGNL SAVSSSEG TIETLNEASKELPERATNPFVNRDLAEFSELEYS 286
Db    183 ----- 182

Qy    287 EMGSSFKGSPKGESAILVENTKEEVI VRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEK 346
Db    183 ----- 182

Qy    347 TMDIFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLED 406
Db    183 ----- 182

Qy    407 SLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTS 466
Db    183 ----- 182

Qy    467 ENKTDEKKIEERKAQIIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEG 526
Db    183 ----- 182

Qy    527 LTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSP 586
Db    183 ----- 182

Qy    587 VLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALK 646
Db    183 ----- 182

Qy    647 ALGTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVP 706
```

Db 183 ----- 182
 Qy 707 EHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSAS 766
 Db 183 ----- 182
 Qy 767 PQELGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNNTAIYSNDDLSSKEDK 826
 Db 183 ----- 182
 Qy 827 IKESETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCL 886
 Db 183 ----- 182
 Qy 887 ELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTK 946
 Db 183 ----- 185
 Qy 947 EAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFS 1006
 Db 186 ----- 216
 Qy 1007 IVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA 1066
 Db 217 IVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA 276
 Qy 1067 LGHVNSTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLTLLILALISLFSIPVIY 1126
 Db 277 LGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLTLLILALISLFSVPVIY 336
 Qy 1127 ERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
 Db 337 ERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373

RESULT 10

US-09-765-205-6

; Sequence 6, Application US/09765205

; Patent No. US20020034800A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Li

; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES

; FILE REFERENCE: 1458.004/200130.449

; CURRENT APPLICATION NUMBER: US/09/765,205

; CURRENT FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: US/09/212,440

; PRIOR FILING DATE: 1998-12-16

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 6

; LENGTH: 373

; TYPE: PRT

; ORGANISM: human

US-09-765-205-6

Query Match

20.4%; Score 1191; DB 9; Length 373;

Best Local Similarity 27.8%; Pred. No. 1.4e-52;
Matches 327; Conservative 12; Mismatches 20; Indels 818; Gaps 7;

```
Qy      1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
      |||: || |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db      1 MEDLDQSPLVSSS-DSPRRQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEEVLERK 58

Qy     61 PAAGLSAAAVP--PAAAPLLDFFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
      |||| || || || |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVP 118

Qy    116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPIAE-----PAAPPSTPAAPKR 166
      ||| ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178

Qy    167 RGSGSVDETLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL 226
      |||
Db    179 RGSS----- 182

Qy    227 SPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYS 286
Db    183 ----- 182

Qy    287 EMGSSFKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEK 346
Db    183 ----- 182

Qy    347 TMDIFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLED 406
Db    183 ----- 182

Qy    407 SLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTS 466
Db    183 ----- 182

Qy    467 ENKTDEKKIEERKAQIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEG 526
Db    183 ----- 182

Qy    527 LTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSP 586
Db    183 ----- 182

Qy    587 VLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALK 646
Db    183 ----- 182

Qy    647 ALGTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVP 706
Db    183 ----- 182

Qy    707 EHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSAS 766
Db    183 ----- 182

Qy    767 PQELGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNNTAIYSNDDLSSKEDK 826
```


Db 183 ----- 182

Qy 827 IKESETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCL 886

Db 183 ----- 182

Qy 887 ELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTK 946

Db 183 -----GSV----- 185

Qy 947 EAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFS 1006

Db 186 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFS 216

Qy 1007 IVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSA 1066

Db 217 IVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSA 276

Qy 1067 LGHVNSTIKELRRLFLVDDLVDLSKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIY 1126

Db 277 LGHVNCTIKELRRLFLVDDLVDLSKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIY 336

Qy 1127 ERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163

Db 337 ERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373

RESULT 11

US-09-893-348-24

; Sequence 24, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: IL 124500

; PRIOR FILING DATE: 1998-05-19

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 24

; LENGTH: 373

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-893-348-24

Qy 767 PQELGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLLSSKEDK 826
 Db 183 ----- 182
 Qy 827 IKESETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCL 886
 Db 183 ----- 182
 Qy 887 ELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTK 946
 Db 183 ----- ||: GSV----- 185
 Qy 947 EAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFS 1006
 Db 186 ----- |||||VVDLLYWRDIKKTGVVFGASLFLLLSLTVFS 216
 Qy 1007 IVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA 1066
 Db 217 IVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA 276
 Qy 1067 LGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIY 1126
 Db 277 LGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIY 336
 Qy 1127 ERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
 Db 337 ERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373

RESULT 12

US-10-060-036-72

; Sequence 72, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Persing, David H.

; APPLICANT: Hepler, William T.

; APPLICANT: Jiang, Yuqiu

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

; FILE REFERENCE: 210121.566

; CURRENT APPLICATION NUMBER: US/10/060,036

; CURRENT FILING DATE: 2002-01-30

; NUMBER OF SEQ ID NOS: 4560

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 72

; LENGTH: 373

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-060-036-72

Query Match 20.4%; Score 1191; DB 15; Length 373;

Best Local Similarity 27.8%; Pred. No. 1.4e-52;

Matches 327; Conservative 12; Mismatches 20; Indels 818; Gaps 7;

Qy	1	MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEELEVLERK	60
Db	1	MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEELEVLERK	58
Qy	61	PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P	115
Db	59	PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSSTVP	118
Qy	116	APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR	166
Db	119	APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR	178
Qy	167	RGSGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL	226
Db	179	RGSS-----	182
Qy	227	SPLSTVSFKEHGYLGNL SAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYS	286
Db	183	-----	182
Qy	287	EMGSSFKGSPKGESAILVENTKKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEK	346
Db	183	-----	182
Qy	347	TMDIFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLED	406
Db	183	-----	182
Qy	407	SLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPILLEDHTS	466
Db	183	-----	182
Qy	467	ENKTDEKKIEERKAQII TEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEG	526
Db	183	-----	182
Qy	527	LTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSP	586
Db	183	-----	182
Qy	587	VLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALK	646
Db	183	-----	182
Qy	647	ALGTKEGIKEPESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVP	706
Db	183	-----	182
Qy	707	EHAELVEDSSPESEPVDFLSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSAS	766
Db	183	-----	182
Qy	767	PQELGKPYLESFQPNLHSTKDAASNIDPTLTKEKISIQMEEFNTAIYSNDDLSSKEDK	826
Db	183	-----	182
Qy	827	IKESETFSDSSPIEII DEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCL	886

Db 183 ----- 182
 Qy 887 ELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTK 946
 Db 183 -----GSV----- 185
 Qy 947 EAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFS 1006
 Db 186 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFS 216
 Qy 1007 IVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA 1066
 Db 217 IVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA 276
 Qy 1067 LGHVNSTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLTLLILALISLFSIPVIY 1126
 Db 277 LGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLTLLILALISLFSVPVIY 336
 Qy 1127 ERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
 Db 337 ERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373

RESULT 13

US-09-893-348-21

; Sequence 21, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: IL 124500

; PRIOR FILING DATE: 1998-05-19

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 21

; LENGTH: 199

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-09-893-348-21

Query Match 15.8%; Score 925; DB 9; Length 199;
 Best Local Similarity 99.0%; Pred. No. 1.7e-39;

	Matches	189;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	973		KTSVVDLLYWRDI		KKTGVVFGASL		FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI		1032	
Db	9		KDKVVDLLYWRDI		KKTGVVFGASL		FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI		68	
Qy	1033		QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKF		1092					
Db	69		QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKF		128					
Qy	1093		AVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQ		1152					
Db	129		AVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQ		188					
Qy	1153		AKIPGLKRKAD		1163					
Db	189		AKIPGLKRKAD		199					

Query Match 15.5%; Score 908; DB 9; Length 199;
Best Local Similarity 96.3%; Pred. No. 1.2e-38;
Matches 184; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 973 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1032
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 9 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 68

[illegible]

RESULT 15

```

US-09-789-386-4
; Sequence 4, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 289
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (31)(138)
US-09-789-386-4

```

Query Match 15.2%; Score 888; DB 9; Length 289;
Best Local Similarity 63.9%; Pred. No. 2e-37;
Matches 184; Conservative 34; Mismatches 58; Indels 12; Gaps 5;

Qy	195	MDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLGNLSAVSSSEGTIE	254
		: : : :	
Db	3	MDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQ	62
Qy	255	ETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGESAILVENTKEEVIVR	314
		: : : : : : :	
Db	63	ENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAVIVANPREEIIVK	122
Qy	315	SKDKED-LVCSAALHSPQESPVG-----KEDRVVSPEKTMDFNEMQMSVVPVREEYAD	368
		: : : : :	
Db	123	NKDEEEKLVSNNILHXQQELPTALTCLKVEDEVVSSEKAKDSFNEKRVAVEAPMREEYAD	182

Qy 369 FKPFEQAWEVKDTYEGSRDVLAA-----RANVESKVDRKCLEDSELEQSLGKDSEGRNEDA 424
 |||||: |||||: | | |: ||| : |: |||||: || | ||||| : |||| | :|
 Db 183 FKPFERVWEVKDSKEDS-DMLAAGGKIESNLESKVDDKKCFADSLEQTNHEKDSSESNDDT 241
 Qy 425 SFPSTPEPVKDSSRAYITCASFT-SATESTTANTFPILLEDHTSENKTD 471
 |||||: || | ||||| | : |||| | |||| | |||||
 Db 242 SFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLGDPTSENKTD 289

Search completed: December 19, 2003, 15:42:41
 Job time : 45 secs

OM protein - protein search, using sw model

Run on: December 19, 2003, 15:33:28 ; Search time 27 Seconds
 (without alignments)
 4142.377 Million cell updates/sec

Title: US-09-830-972-2
 Perfect score: 5848
 Sequence: 1 MEDIDQSSLVSSSTDSPRP.....VKDAMAKIQAKIPGLKRRKAD 1163

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_76:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	789.5	13.5	776	2	A46583	neuroendocrine-spe
2	685	11.7	208	2	I60904	neuroendocrine-spe
3	671	11.5	267	2	A60021	tropomyosin-relate
4	517	8.8	2484	2	T26216	hypothetical prote
5	503.5	8.6	2607	2	T26215	hypothetical prote
6	328.5	5.6	5327	2	T13564	microtubule-associ
7	322	5.5	7962	2	I38346	elastic titin - hu
8	320	5.5	222	2	T26213	hypothetical prote
9	304.5	5.2	873	2	A47283	calphotin - fruit
10	302.5	5.2	1829	2	T24583	hypothetical prote
11	295.5	5.1	865	2	A47282	calcium-binding pr
12	292	5.0	3507	2	T34513	hypothetical prote
13	291.5	5.0	2364	2	A56577	microtubule-associ

14	288.5	4.9	971	2	T19431	hypothetical prote
15	284	4.9	2464	1	QRMSPI	microtubule-associ
16	281	4.8	3488	2	T34418	hypothetical prote
17	279.5	4.8	1262	2	T22523	hypothetical prote
18	277	4.7	1621	2	A82255	hypothetical prote
19	275.5	4.7	3924	2	S37431	ankyrin 2, neurona
20	275	4.7	1299	2	T47182	hypothetical prote
21	273.5	4.7	1029	2	T30351	mucin-like protein
22	273.5	4.7	1274	2	T16251	hypothetical prote
23	273	4.7	1558	2	B71603	RESA-H3 antigen PF
24	272.5	4.7	3534	2	T42567	tegument protein 2
25	270	4.6	1230	2	T22458	hypothetical prote
26	269.5	4.6	2187	2	T30826	nascent polypeptid
27	267	4.6	1684	2	JW0057	gravin - human
28	265.5	4.5	1828	2	A40115	microtubule-associ
29	263	4.5	1825	2	S13507	microtubule-associ
30	261.5	4.5	1087	1	QFMSH	neurofilament trip
31	261	4.5	606	2	A43427	neurofilament trip
32	261	4.5	2570	2	T17451	fimbriae-associate
33	260	4.4	1804	2	T34518	nestin - golden ha
34	259.5	4.4	1020	1	QFHUH	neurofilament trip
35	259	4.4	1510	2	T33100	hypothetical prote
36	258.5	4.4	1830	2	A37981	microtubule-associ
37	257	4.4	1224	2	T14007	microtubule-associ
38	256	4.4	2361	2	T25752	hypothetical prote
39	254.5	4.4	6642	2	T29757	protein UNC-89 - C
40	254	4.3	1616	2	G64242	cytadherence-acces
41	254	4.3	3381	2	T42389	versican precursor
42	253	4.3	3421	1	WZBEB6	367K tegument prot
43	252.5	4.3	5170	2	T15348	hypothetical prote
44	251	4.3	1824	1	QRHUMT	microtubule-associ
45	250.5	4.3	4377	2	A55575	ankyrin 3, long sp

ALIGNMENTS

RESULT 1

A46583

neuroendocrine-specific protein, splice form A - human

N;Contains: neuroendocrine-specific protein, splice form B

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: A46583; I60903

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: A46583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-776 <ROE1>

A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307

A;Accession: I60903

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 421-776 <ROE2>
A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309
C;Genetics:
A;Gene: GDB:RTN1; NSP
A;Cross-references: GDB:203968; OMIM:600865
A;Map position: 14q21-14q22

Query Match 13.5%; Score 789.5; DB 2; Length 776;
Best Local Similarity 31.2%; Pred. No. 3.4e-25;
Matches 243; Conservative 115; Mismatches 252; Indels 169; Gaps 28;

```

Qy      487 TSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGT 546
      : | : | | : : : : : | : | | : | : | :
Db      65 SGPARQSP--VAMETASTGVAGVSSAMDHTFSTTSKDGE-----SCYTSLI-----S 110

Qy      547 KIAYETKVDLVQTSEAIQ-ESLYPTAQLCPSFEEAEATPSPVLPDI--VMEAPLNS---- 599
      | | : | : : | : | : | | | | : : | |
Db      111 DICYPQEDSTYFTGILQKENGHVITISEP---EELGTPGPSLPDVPGIESRGLFSSDSG 167

Qy      600 --LLPSAGASVVQPSVSPLEAPPPVSY-----DSIKLEPENPPPYEEA-----M 641
      : | : | : | : | : : | : : : : | :
Db      168 IEMTPAESTEVNKKILADPLDQMAEAYKYIDITRPEEVKHQEQHHPELEDKDLDFKNKDT 227

Qy      642 NVALKALGTKEGIKEPE-----SFNAAVQETEAPYISACDLIKETKLSTE-PSP 690
      : : : | | : : | : : : : | | | | | : | : : : : |
Db      228 DISIK----PEGVREPDKPAPVEGKIIKDHLLEESTFAPYID--DLSEEQRRAPIITTP 280

Qy      691 DFSNYSEIAKFEKSVPEHAELVEDSSPESEPVDLF-SDDSIPEV----PQTQEEAVMLMK 745
      : | | : : : | : : : | | : : | : : :
Db      281 VKITLTEIE-----PSVETTTQEKTPKQDICKLPSPDTPVPTVTVSEPEDDSPGSITPP 334

Qy      746 ESLTEVSETVAQHK-----EERLSASPQELGKPYLESFQP----NLHSTKDAASND---- 792
      | | | : | : : | : : | : | : | : : :
Db      335 SSGTEPSAAESQGKGSISEDELITAIKEAKGLSYETAENPRPVGQLADRPEVKARSGPPT 394

Qy      793 IPTLTKEKISLQMEEFNNTAIYSNDDLLSSKEDKI----- 827
      | : | : : : : | : : : | : :
Db      395 IPSPLDHEASSAESGDSEIELVSEDPM--AAEDALPSGYVSFGHVGGPPPPSPASPSIQYS 452

Qy      828 ---KESETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEI-----ANIQSG 879
      : | | | : | : | : : | : : : : : :
Db      453 ILREEREAE LDS---ELIIESCDASSASEESPKREQDSPPMKPSALDAIREETGVRAEER 509

Qy      880 ADSLPCLELPCDLSFKNIYPKDEVHVSDEFSENRRSSVSKASISPSNVSALEPQTEMGSIV 939
      | | | | : | : | : | : | : | : | :
Db      510 APSRRGLAEPG--SFLD-YPSTEPQGPPEL-----PPGDGALEPETPM---- 549

Qy      940 KSKSLTKEAEKKLPDTEKEDRSLSAVLSAE-----LSKTSVVDLLYWRD 984
      | | : : | : : : : : : : : : | : | : | : |
Db      550 -----LPRKPEEDSSSNQSPAATKGPGLPGAPPPLLFLNKQKAIDLLYWRD 597

Qy      985 IKKTGVVFGASLFLLLSLTVFSIVSVIAYIALALLSVTISFRIYKGVIAIQKSDEGHFP 1044
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db      598 IKQTGIVFGSFLLLSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGHFP 657

```

Qy 1045 RAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGA 1104
 Db 658 KAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLMWLLTYVGA 717

Qy 1105 LFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRRKAD 1163
 Db 718 LFNGLTLLLMAVVSMTPLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIPGAKRHAE 776

RESULT 2

I60904

neuroendocrine-specific protein C - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: I60904

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: I60904

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-208 <RES>

A;Cross-references: GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

Query Match 11.7%; Score 685; DB 2; Length 208;
 Best Local Similarity 67.0%; Pred. No. 1e-21;
 Matches 128; Conservative 32; Mismatches 31; Indels 0; Gaps 0;

Qy 973 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1032
 Db 18 KSQAIDLLYWRDIKQTGIVFGSFLLLSLTQPSVSVVAYLALAALSATISFRIYKSVL 77

Qy 1033 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLK 1092
 Db 78 QAVQKTDEGHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLK 137

Qy 1093 AVLWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQ 1152
 Db 138 AVLWLLTYVGALFNGLTLLLMAVVSMTPLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQ 197

Qy 1153 AKIPGLKRRKAD 1163
 Db 198 AKIPGAKRHAE 208

RESULT 3

A60021

tropomyosin-related protein, neuronal - rat

C;Species: Rattus norvegicus (Norway rat)

Qy 28 FVTEPEDEE---DEEEEEDEEED-----DEDLEELEVL----- 57
 | | | : | : | | | | | | : | : |
 Db 1437 FGTESSEESQKADGNQENQEEEDVVAELNFHPIRQWRDEDVISLQSLKSLVAEVCITDV 1496
 Qy 58 -----ERKPAAGLSAAAVPPAAAPL-LDFSSDSVPPAPRGPLPAAPPAAP--ERQPSW 108
 | : : | | : : | | | : | | : | | |
 Db 1497 DASDVNEQDEESTLKILKVVVPSEPSLLELDFTND--PKVIHVPIPLMEPATMYLEEMVEW 1554
 Qy 109 -----ERSPAAPAPSLPPAAAVLPS-----KLP-EDDEPPARPPPPPPA 146
 | : | | : : : | | | | | | | | |
 Db 1555 IIADAVKEVSEMEVVTSEISEMAPQVSESTCPIPEPLADLKLPVEDDEKTPEPEPVVPG 1614
 Qy 147 GASPLAEPAPSTPAAPKRRGSGSVDETFLFALPAASEPVIPS-SAEKIMDLMEQPGNTV 205
 | | | | | | : | | | | | : | : | | |
 Db 1615 QVQERIIPIEVEQAPTIPQRPPRAPKSE----LPKVAKPLDDSKSRVRFAPLNIKLGRTY 1670
 Qy 206 SSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLGNL SAVSSSEG TIEETLNEASKELP 265
 | | : | | | | | : : : : : | : |
 Db 1671 SEEQK-----ELVESLE--RPLTIIT-----QOKPP 1695
 Qy 266 ERAT-----NPFVNRDLAEFSELEYSEMGS SPKSGESAILVENTKKEEVIVRSKDKE 319
 | : | : | | | : | : | | |
 Db 1696 EKPTEDIGALSPLSPNTLAEYEEVPMMDMQS----- 1726
 Qy 320 DLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQ-MSVVAPVREEYADFKPFQAWEV 378
 | | | | | : : : | : | | | | | | | |
 Db 1727 -----VPHSPQE-----KQEEI---EALSEIIEEPQAMKEVE-----KPVESAPE- 1763
 Qy 379 KDTYEGSRDVLAAARANVESKVDRCLEDL--EQKSLGKDSEGRNEDASFPSTPEPVKDS 436
 | | : | | : : | : : | | : | : |
 Db 1764 KD-----NESLEAPEIINEPIRRVLVETKIMGPGKSLNED----NDD----- 1801
 Qy 437 SRAYITCASFTSATES'TTANTFPLLEDHTSENKTDEKKIEERKAQIIITEKTSPKTSNPFL 496
 : | | | : | | : | | | | |
 Db 1802 -----DDGSECLDSIGDL SER-----TIQRFN 1824
 Qy 497 VAVQDSEADYVTTDTLSKVT-----EAAVSNMPEGLTPDLVQEACESELNEATGTKI 548
 : : | : : | : : | : : | : : |
 Db 1825 TSIDDPS---IRRDSFSSISSFGDRQKFRTAIENIRQDLLP----- 1862
 Qy 549 AYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASV 608
 : : | : : | : | | : : : | : | : |
 Db 1863 -FQSSV-----SQYLRSSPNPSQQL-----LVTNLSMDSP-SDLSPNA---- 1898
 Qy 609 VQPSVSPLEAPPPVSYDSI-----KLEPENPPPYEEAMNVALKALGTKEGIKEPESFNAA 663
 | | : : | : | : | : : : : :
 Db 1899 -----PPVGFENTAQFLEKLQQEDRPSAEGSID-----SSGFEKVD--HEG 1937
 Qy 664 VQETEAPYISIACDLIKETKLSTEPSPDF-----SNYSEIAKFEKSVPE 707
 : | | : : : : | | : : : | : |
 Db 1938 LDEFAAPPVH---DPMQKSVFGSLGSDDMKPGSQDDGFVFIERNEANEATLKNQKMSSH 1994
 Qy 708 HAEIVEDS-----SPESEPVDLFSDDSIPEVPQTQEEAV---MLMKESLTE 750
 | : : | : | : | : : : : : : :
 Db 1995 HNDVIEKNYFNDNAPTAALLESPIAEEARKLVQDAVESASEYKKQAVDSGDEIGRELLDN 2054

Qy 751 VSETVAQHKE-----ERLSASPQELGKPYLESFQP 780
 | : : | || | : : : | : : : |
 Db 2055 VEQKIEQVKPEIVDSLHKAYDGVGDFVHETVPNAVDDFVREAEKQLPESPVPEKIETPEP 2114

 Qy 781 --NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDK-----IKES 830
 : : | | : : : : | : : | : : : :
 Db 2115 LVDIHDTVDKVHDEVDFNRLREP-----TPPFETDDVAPLSDDKPQFGNQTPPEEDE 2165

 Qy 831 ETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGA----DSLPLCL 886
 || | : | : | : : : : : | : | : || : ||
 Db 2166 TTFDRKGPLTIPPEVEKAAAAQNND---LDDFDPLVTSNTGAAGAAVGAAGAAVESLTEE 2222

 Qy 887 ELPCDLSFKNI-----YPKDEVHVSDEFSENRSSVSKASISPSNVSA-----LEPQTEM 935
 | : | : : || : || : || | : | :
 Db 2223 EMFGHQKFETVPRPPTPKD---ISDE-----DVKPSTVNLGPSHHHSHPSPPH 2268

 Qy 936 GSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGAS 995
 || : | : : | : : | : : || : || : :
 Db 2269 HSILKHHG-----DAWIDFKTVPPCVLDVIYWRDAKKSIVLSLA 2308

 Qy 996 LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAIS 1055
 | : | | : : : | | | | : : | | : : | | | : : :
 Db 2309 LLVLFVLAKYPLLTVVVTYSLLLALGAAAGFRVFKKVEAQIKKTDSEHPFSEILAQDLTLP 2368

 Qy 1056 EELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILA 1115
 : | | : : : | : : : | : : : | : : | : | : |
 Db 2369 QEKVHAQADVFVEHATCIANKLKKLVFVESPLESIKFGVLVLSLTYIASWFSGFTLAILG 2428

 Qy 1116 LISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLK 1159
 | : : || : | : | | : : : | : | :
 Db 2429 LLGVFSVPKVYESNQEAIDPHLATISGHLKNVQNIIDEKLPFLR 2472

RESULT 5

T26215

hypothetical protein W06A7.3a - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26215

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26215

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2607 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3a

A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2; 2586/2

Query Match 8.6%; Score 503.5; DB 2; Length 2607;
 Best Local Similarity 20.8%; Pred. No. 1e-12;
 Matches 280; Conservative 181; Mismatches 481; Indels 407; Gaps 52;

Qy 28 FVTEPEDEE---DEEEEEDEED-----DEDLEELEVL----- 57
 | | | : | : | | | | | : | : |
 Db 1437 FGTESSEESQKADGNQENQEEEDVVAELNFHPIRQWRDEDVISLQSLKSLVAEVCITDV 1496
 Qy 58 -----ERKPAAGLSAAAVPPAAAAPL-LDFSSDSVPPAPRGPLPAAPPAAP--ERQPSW 108
 | : : | | : : | | | : | | : | | | |
 Db 1497 DASDVNEQDEESTLKILKVVVSEPSLLELDFTND--PKVIHVPIPLMEPATMYLEEMVEW 1554
 Qy 109 -----ERSPAAPAPSLPPAAAVLPS-----KLP-EDDEPPARPPPPPPA 146
 | : | | : : : | | | | | | | | | |
 Db 1555 IIADAVKEVSEMEVVTESEISEMAPQVSESTCPIPEPLADLKLPVEDDEKTPEPEPVVPG 1614
 Qy 147 GASPLAEPAPSTPAAPKRRSGSVDETLFALPAASEPVIPS-SAEKIMDLMEQPGNTV 205
 | | | | | : | | | : | : | : | : | : |
 Db 1615 QVQERIIPIEVEQAPTIPQRPPRAPKSE----LPKVAKPLDDSKSRVRFAPLNIKLGRTY 1670
 Qy 206 SSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLGNL SAVSSSEG TIEETLNEASKELP 265
 | | : | | | | : : : : : : : : : :
 Db 1671 SEEQK-----ELVESLE--RPLTIIT-----QQKPP 1695
 Qy 266 ERAT-----NPFVNRDLAEFSELEYSEMGSFSGSPKGESAILVENTKKEEVIVRSKDKE 319
 | : | : | | | : | : | | : : | : | : |
 Db 1696 EKPTEDIGALSPLSPNTLAEYEEVPMMDM-QSVPHSP-----QEKQEEIEALSEIIE 1746
 Qy 320 DLVCSAALHSPQES-PVGKEDRVVSPEKTMDFNEMQMSVVAPVREEYADFK---PFEQA 375
 : : | | | : : : | | | : | : | :
 Db 1747 EPQAMKEVEKPVESAPEKDNESELAPE---IINE-----PIRRVLVETKIMGPGKSL 1795
 Qy 376 WEVKDITYEGSRDVLAAANVESKVDKCLEDSLEQKSLGKDS-----E 418
 | | : : | : : : : : | : | : : |
 Db 1796 NEDNDDDDGSECLDSIGDLSSERTIQR-FNTSIDDPSIRRDSSFSSISSFGDRQKFR TAIE 1854
 Qy 419 GRNED-----ASFPSTPEPVKDSSRAYITCASFTSATESTT-----ANTFPLLE 462
 : | | : | | : : | | : : : | | |
 Db 1855 NIRQDLLPFQSSVSQYLRSSPNP---SQQLLVTNLSMDSPDLSPNAPPVGFENTAQFLE 1911
 Qy 463 -----DHTSENKTDEKKIEERKAQII-----TEKTSPKTSNPF 495
 | : | | : : | | : : : : : : : :
 Db 1912 KLQQEDRPSAEGSIDSSGFKEVDHEGLDEFAAPPVHDPMQKSVFGSLGSDDMKPGSQDDG 1971
 Qy 496 LVAVQDSEADYVT-----TDTLSK-----VTEAAVSNMPEGLTPDLVQ 533
 | : : | : | : | : : : : : : :
 Db 1972 FVFIERNEANEATLKKNQKMSSHNDVIEKNYFNDNAPTAALLESPIAEEARKLVQDAVE 2031
 Qy 534 EACE-----SELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVL 588
 | | : : | : : | | | : : | | : |
 Db 2032 SASEYKKQAVDSGDEIGRELLDNVEQKIEQVKEPIVDSLHKAYDGVGVFVH-ETVNAV- 2089
 Qy 589 PDIVMEAPLNSLLPSAGASVVQPSVSPL EAPPPVSYSIKLEPENPPPYEEAMNVALKAL 648
 | | | | | | | : | |
 Db 2090 DDFVREAE-----KQLPESPVP----- 2106
 Qy 649 GTKEGIKEPESFNAAVQETEAPYISIACDLIK-----ETKLSTEPSPDFS NYSEIAKFEK 703
 | | : | | : | : | : | : | : |
 Db 2107 ---EKIETPE-----PLVDIHDTVDKVHDEVNDFLRREPTPPFE----- 2142

Qy 704 SVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLT---EVSETVAQHKE 760
 Db 2143 -----TDDVAPLSDDKPQFGNQT-PE----EDETTFDRKGPLTIPEEVEKAAAAQNN 2189

Qy 761 ERLSASPQELGKPYLESFQPNLHSTKDA-----ASNDIPTLTKEKISLQMEEFNIAI 813
 Db 2190 D-----LDDFDPLVTSNTGAAFGAAVGAAAIVESLTEEEMFGHQ--KFETVP 2234

Qy 814 YSNDDLLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDSP--KLAKEYTDLEVSDKS 871
 Db 2235 RPPTPKDISDEDVKPS-----TVNLGPSHHHSHPSPPHHSILKHGDAWIDFKT 2284

Qy 872 EIANIQSG-----ADSLPCLE---LPCDLSFKNIYPKDEVH 904
 Db 2285 VPPCAQNAFSPGEIMFLLAFFVYLSCFASFFSKSLPLLDNLLSLVLYSISLI-----IH 2339

Qy 905 VSDE-----FSENRSSVSKASISPSNVSA-----LEPQTEMGSIKSKSLTKEAEK 950
 Db 2340 VKHHRKFRWNEEQATTMSKLGAVGRGLYALIAFIVNIVLRVGLNVALVVGVAVSAHEAYK 2399

Qy 951 KLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSV 1010
 Db 2400 LTKS-----SGVLRKKEVLDVIYWRDAKSAIVLSLALLLVFLAKYPLLTV 2446

Qy 1011 TAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHV 1070
 Db 2447 VTYSLLLALGAAAGFRVFKKVEAQIKKTSEHPFSEILAQDLTLPQEKVHAQADVFVEHA 2506

Qy 1071 NSTIKELRRLFLVDDLVDLSKFAVLMWVFTYVGFALFNGLTLLILALISLFSIPVIYERHQ 1130
 Db 2507 TCIANKLKLKLVFVESPLESIKFGVLVWSLTYIASWFSGFTLAILGLLGVSVPKVIYESNQ 2566

Qy 1131 VQIDHYLGLANKSVKDAMAKIQAKIPGLK 1159
 Db 2567 EAIDPHLATISGHLKNVQNIIDEKLPFLR 2595

RESULT 6

T13564

microtubule-associated protein homolog - fruit fly (*Drosophila melanogaster*)

N;Alternate names: hypothetical protein EG:49E4.1

C;Species: *Drosophila melanogaster*

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C;Accession: T13564

R;Spanos, L.; Papagiannakis, G.; Siden-Kiamos, I.; Louis, C.

submitted to the EMBL Data Library, April 1999

A;Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.

A;Reference number: Z17689

A;Accession: T13564

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5327 <SPA>

A;Cross-references: EMBL:AL031128; PIDN:CAA20006.1

C;Genetics:

A;Cross-references: FlyBase:FBgn0025392

A;Introns: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5272/1

A;Note: EG:49E4.1

C;Superfamily: Drosophila 576K microtubule-associated protein homolog

Query Match 5.6%; Score 328.5; DB 2; Length 5327;
Best Local Similarity 22.7%; Pred. No. 4.1e-05;
Matches 255; Conservative 176; Mismatches 453; Indels 238; Gaps 54;

```
Qy      2 EDIDQSSLVSSSTDSPPRPPPAFKYQFVTEP----EDEEDEEEEEDEEEDDEDLEELEVL 57
      :: ||| | : || | : | | : || | : || | : | | |
Db    3196 DEADKSKEESRRESGAEKSPLASKE--ASRPASVAESIKDEAEKSKEESRRESVAEKSPL 3253

Qy      58 ERKPAAGLSAAA--VPPAAAPLLDFSSDSVPPAPRGPLPAAPPAAP----- 102
      | | : : | | : | ||| | : || : : |
Db    3254 PSKEASRPTSAKSVKDEAEKSKEESSRDSV--AEKSPLASKEASRPASVAESVQDEAEK 3311

Qy     103 -----ERQPSWERSPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLA-EPAA 156
      | : | : || | : | | : | | : : | ||| : | :
Db    3312 SKEESRRESVAEKSPLAYKEASRP-ASVAESIKDEAEKSKEESRRESVAEKSPLASKEAS 3370

Qy     157 PPSTPA-----APKRRGSGSVDETLFALPAAS-EPVIPSS-AEKIMDLMEQPGNTVSSG 208
      | : : | | : | | | ||| | : || | : | :
Db    3371 RPTSVAESVKDEAEKSKEESSRDSVAEKSPLASKEASRPASVAESVQDEAEKSKEESRRE 3430

Qy     209 QEDFPSVLLETAASLPSLSPLSTVSFKEHG-----YLGNL SAVSSSEG TIEETLNEAS 261
      | | | | : | | : | : | : | : : | : : | :
Db    3431 SVAEKSPLASKEASRPASVAESVKDDAEKSKEESRRESVAEKSPLASKEASRPASVAESV 3490

Qy     262 KELPERATNPFVNRDLAEFSELEYSEMG--SSFKGSPKGESAILVENTKEEVIVRSKDKE 319
      | : | : : || | | : | | | : | : ||| : |
Db    3491 KDEAEKSKEESRRESVAEKSPLPSKEASRPTSVAESVKDEA----EKSKEE-----SRRE 3541

Qy     320 DLVCSAALHSPQES-PVGKEDRVV-SPEKTMDIFNEMQMSVVAPVREEYADFKPFEQAW 377
      : : : | | : | | : | || : : : : | : : | |
Db    3542 SVAEKSSLASKEASRPASVAESVKDEAEKSKEESRRESVAEKSPLASKEAS-RPASVAES 3600

Qy     378 VKDTYEGSRDV-----LAARANVESKVDRK--CLEDSLEQKSLGKDSEGRNE----- 422
      ||| | | : : | : : | | : : : | : : | | |
Db    3601 VKDEAEKSKEVSRRESVAEKSPLPSKEASRPTSVAESVKDEADKSKEESRRESGAEKSPL 3660

Qy     423 ---DASFP-STPEPVKDSSRAYITCASFTSATESTTANTFPILLEDHTS-----ENKTD- 471
      : || | | | ||| : : : | | | : || | | : | |
Db    3661 ASMEASRPTSVAESVKDETEK----SKEESRRESVTEKS-PLPSKEASRPTSVAESVKDE 3715

Qy     472 -EKKIEERKAQIITEKT---SPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEG- 526
      || || : : : || : | : | | | : : : : | : : |||
Db    3716 AEKSKEESRRESVAEKSPLASKESSRP-----ASVAESIKDEAEGTKQESRRESMPESG 3769

Qy     527 -----LTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYP 569
      || | | : : | : | : | | : | : | : |
Db    3770 KAESIKGDQSSLASKETS RPD SVVESVKDETEKPEGSAI---DKSQVASRPESVAVSAKD 3826

Qy     570 TAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKL 629
      | | : | | || || | || : : || : | | |
Db    3827 EKSPLHSRPESVADKS---PDASKEA-----SRSLSAETASSPIEEGPRSIAD---- 3872

Qy     630 EPNPPPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPS 689
      : : : | | : | | : : : | : : | | : |
Db    3873 -----LSLPLNLTGEAKG-KLP-TLSSPIDVAEGDFL-----EVKAESSPR 3911
```


Db 6634 KKKEAPPAKVPEVPKKPEEKVPVLI PKKEKPPPAKVPEVPKKPVPEEKVPVPVPPKKVEAP 6693

Qy 99 PA-APE--RQPSWERSPAAPAP---SLPPA-AAVLPSKL-PEDDEP---PAR---PPPPP 144
 || || :| | : || | :| || || :| | : ||

Db 6694 PAKVPEVPKKPVPEKKVPVPAPKKVEAPPAKVPEVPKKLIPEKKKPTVPVPPKKVEAPPPKV 6753

Qy 145 PAGASPLAEPAPSTPAAPKRRGSGSVDETFLFALPAASEPVI PSSAEKIMDLMEQPGNT 204
 | : | | : | || : :| | : : | :

Db 6754 PKKREVPVPVVALPQE-----EEVLF-----EEEIVPE--EEVLPPEEEE---- 6790

Qy 205 VSSGQEDFPSVLLETAASLP---SLSPLSTVSFKEHGYLGNL SAVSSSEGTI--EETLNE 259
 | :| : || | || : | | | : | | | |

Db 6791 VLPPEEEE--VLPPEEEVLPPEEEI PPEEEVPPEEEY-----VPEEEEFVPEEEVLPE 6841

Qy 260 ASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGESA-----ILVENTKEEVIV 313
 :| | | : : : | : || | | : : :| : | :

Db 6842 VKPKVPVPAPVPEIKKKVTEKKVV-----IPKKEEAPPAKVPEVPKKVVEEKRII 6890

Qy 314 RSKDKEDLVCSAALHSPQESPVGKED-----RVVSPEKTMDFNEM----- 354
 | :| | | :| | :| :| : : : | : : :

Db 6891 LPKEEEVLPVEVT-EEPEEEPISEEEIPEEPPSIEEVEEVAPPRVPEVIKKAVPEAPTVP 6949

Qy 355 -----QMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESK 398
 : | || : : | | : || : : : |

Db 6950 PKKVEAPPAKVSKPIPEEKVPVPVQKKEA---PPAKVPEVPKKVPEKKVLVPKKEAVPPA 7006

Qy 399 VDRKCLEDSE-----LEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCA 444
 | || : || : : : | | : | | |

Db 7007 KGRTVLEEKVSVAFRQEVVVKERLELEVVAEVEEI PEEEEFHEVEE-----YFEEG 7058

Qy 445 SFTSATESTTANTFPILLEDHTSEN-----KTDEKKIEER-----KAQIITEKTSPKT 491
 | | : :| :| | : :| : : | | | :| | |

Db 7059 EFHEVEEFIKLEQHRVEEHRVEKVRHVEVFEEAEVEVFEEKPKAPPKGPEISEKIIPPK 7118

Qy 492 SNPFLVAVQDSEADYVTTDTLSKVTEAAV-----SNMPEGLTPDLV----- 532
 | | : | | | | : :| | | | |

Db 7119 KPPTKVVPKKEPPAKVPEVPKKI VVEEKVRVPEEPRVPPTKVPEVLPPKEVVPEKKVPVP 7178

Qy 533 ----QEACESELNEATGTIAETKVDL-----VQTSEAIQESLYP 569
 || : : || : : | || : : : | :| :

Db 7179 PAKKPEAPPPKVPEAP-KEVVPEKKVPVPPPKKEVPPTKVPEVPKAAVPEKKVPEAIPP 7237

Qy 570 TAQLCPS--FEEAEATPS-----PV-LPDI VMEAPLNSLLPSAGASVVQPSVSPLE 617
 : | || | :|| || : : : | :| :| :| :| :

Db 7238 KPESPPPEVFEEPEESPSAPPKKPEVPPVRVPEVPKEVVPEKKVPAAPPK--KPEVTPVK 7295

Qy 618 AP-----PPVSY-----DSIKLEPENPPP--YEE 639
 | || : :| :| :| :| :| :|

Db 7296 VPEAPKEVVPEKKVPVPPPKKEVPPTKVPEVPKVAVPEKKVPEAIPPKPESPPPEVFEE 7355

Qy 640 AMNVALKALGTKEGIKEPESFNAA-----VQETEAPYISIACDLIKETKLSTEP 688
 ||| : | :|| | || | | :| : : | :| :

Db 7356 PEEVALEE-PPAEVVEEPEP--AAPPQVTVPPKNPVPEKKAPAV-----VAKKPELPPVK 7407

Qy 689 SPDFSNYSEIAKFESVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESL 748
 | : | : || || || || : | :||| || :

Db 7408 VPEVP--KEVVP-EKKVP-----LVVPKKPEAPPA-----KVPEVP-----KEVV 7444

Qy	749	TEVSETVAQHKEERLSASPQELGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEE	808
		: : : : : : :	
Db	7445	PEKKVAVPKKPEVPPAKVPEVPKKPVLEE-KPAVPVPERAESPPPEVYEEPEEIAPEEE-	7502
Qy	809	FNTAIYSNDDLSSKEDK---IKESE-----TFSDSSPIEIIDFPTFVSAKDDSPKLA	859
		: : : : : : :	
Db	7503	-----IAPEEEKVPVVAEEEEPEVPPPAVPPEEPKKIPEKKVPVIKKPEAPP-P	7550
Qy	860	KEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFK-NIYPKDEVHVSDEFSENRSSVSK	918
		: : : : : :	
Db	7551	KEPEPEKVIIEKPKLKPRPPPPPPAPPKEDVKEKIFQLKAI PKKKV-----PENPQVPEK	7604
Qy	919	ASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLP--SDTEKEDRSLSAVL	967
		: : : : :	
Db	7605	VELTPLKVPGGE-----KKVRKLLPERKPEPEEEVVLKSVL	7640

Query Match 5.5%; Score 320; DB 2; Length 222;
Best Local Similarity 32.1%; Pred. No. 1e-06;
Matches 59; Conservative 47; Mismatches 78; Indels 0; Gaps 0;

RESULT 9

A47283

calphotin - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000

C;Accession: A47283

R;Ballinger, D.G.; Xue, N.; Harshman, K.D.

Proc. Natl. Acad. Sci. U.S.A. 90, 1536-1540, 1993

A;Title: A *Drosophila* photoreceptor cell-specific protein, calphotin, binds calcium and contains a leucine zipper.

A;Reference number: A47283; MUID:93165730; PMID:8434015

A;Contents: photoreceptor cells

A;Accession: A47283

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-873 <BAL>

A;Cross-references: GB:L05080; NID:g157071; PIDN:AAA28420.1; PID:g157072

A;Note: sequence extracted from NCBI backbone (NCBIN:124958, NCBIPI:124959)

C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; von Willebrand factor type C repeat homology

Query Match 5.2%; Score 304.5; DB 2; Length 873;
Best Local Similarity 21.9%; Pred. No. 3.1e-05;
Matches 213; Conservative 126; Mismatches 362; Indels 273; Gaps 42;

Qy	62	AAGLSAAAVPPAAAPLLDFSSDSVPPAPR--GPLPAAP----PAAP-----ERQPSWER	110
		: :: : :	
Db	11	SAPVAAPVTPSAVAAPVQVVSPAAVAVAPAVVAPAPAAPTAVTPVAPPPTLASVQPATVT	70
Qy	111	SPAAPAP----SLPPAAAVLPSKLPEDDEPPARPPPPPP-----AGASPLAEPAPAP	158
		: : : : : : :	
Db	71	VP-APAPIAAASVAPVASVAPPVVAAPTTPAASPVSTPPVAVAQIPVAVSAPVAPPVAAT	129
Qy	159	STPAAPKRRGSGSVDETLFALP--AASEP---VIPSSAEKIMDLMEQPGNT---VSSGQ	209
		: : : :	
Db	130	PTPVAPI-----PVAAPVIATPPVAASAPTPAAVTPVVSPIATPPVVPANTTVPVAAPV	184
Qy	210	EDFPSVLLETAASL-PSLSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERA	268
		: : :: : : : : :	
Db	185	AAVPAAVPVAPVLAAPAVAPAVAPVVAETPAPPPVAEIPVA--TIPECVAPLIPEVSVVA	242
Qy	269	TNPFVNRDLAEFSELEYSEMSSFKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALH	328
Db	243	TKPLA-----AAEPVVVAPPATETPVVAPAAA	269
Qy	329	SPQESPVGKEDRVVSPEKTMDIFNEMQMSVAPVREEYADFKPFEQAWEVKDTYEGSRDV	388
		: : :	
Db	270	SPHVS-----VAP-----AVETAVVAPV-----	287
Qy	389	LAARANVESKVDRKCLEDLSLEQKSL---GKDSEGRNEDASFPSTPEPVKDSSRAYITCA	444
		: : : : : : : :	
Db	288	---SASTEPPVAAATLTAPETPALAPVVAESQVAANTVVATPPTPAPEPETIAPPVVAE	344
Qy	445	SFTSATESTTANTFPLLEDHTSENKTDEKKIEERKAQIITEKTSPKTSNPFLVAVQDSEA	504
		: : : :: : : : :	

Db 345 TPEVASVAVAETTPPVVPPVAAES-----IPAPVVATTPVPATLAVTDPD- 389
 Qy 505 DYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQ 564
 Db 390 -----VTASAVPELPPVIA PSPVPSA-----VAETPVDLA-----P 420
 Qy 565 ESLYP-TAQLCPSF--EEAEATPSPVLPDI VMEAPLNSLLPSAGASVVQPSVSPLEAP-- 619
 Db 421 PVLPPVAAEPVPAVVAEETPETPAPASAPVTI-AALD--IPEVAPVIAAPSDAPAEAPSA 477
 Qy 620 --PPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIACD 677
 Db 478 AAPIVS-----TPPT-----TASVPETTAPPAAPVTE 504
 Qy 678 -----LIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAE--LVEDSSPESEPVDLFSD-DS 729
 Db 505 PIDVSVLSEAAIETPVAPPVEVTTEVAVADVAPPEAAEDLIEPVEPPAPIPDLLEQTTT 564
 Qy 730 IPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQPNLHSTKDAA 789
 Db 565 VPAVEAAESTSSPIPETSLPPPNEAVA---SPEVAVAPITAPEPIPEP-EP SLATPTEPI 620
 Qy 790 SNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIEIIDEFPTFV 849
 Db 621 PVEAPV-----VIQEAVDAVEVPVTETSTSI PETTVEFPEAV 657
 Qy 850 SAKDDSPKLAKEYTDLEV-SDKSEIANIQSGAD---SLPCLELPCDLSFKNIYPKDEVH 904
 Db 658 AEKVLDP AI----TEAPVTTQEPDVANINDGAPATEITTPAVEI-----VT 699
 Qy 905 VSDEFSENRSSVSKASISPSNVSALE-PQTEM--GSIVKSKSLTKEAEKKLPDTEKEDR 961
 Db 700 AAAEVS DTAIPLIDPPV-PQEI AVAEIPETETKPAEVIVEQS-TIPIEAPVPEVSKYAEP 757
 Qy 962 SLSAVLSAELSKTS 975
 Db 758 VISEAPAAEVPITA 771

RESULT 10

T24583

hypothetical protein T06D8.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T24583

R;Palmer, S.

submitted to the EMBL Data Library, April 1995

A;Reference number: Z19909

A;Accession: T24583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1829 <WIL>

A;Cross-references: EMBL:Z49130; PIDN:CAA88964.1; GSPDB:GN00020; CESP:T06D8.1

A;Experimental source: clone T06D8

C;Genetics:

A;Gene: CESP:T06D8.1

A;Map position: 2

A; Introns: 1391/3; 1432/3; 1470/3; 1505/1; 1520/1; 1616/1; 1644/1; 1687/3; 1742/1

Query Match 5.2%; Score 302.5; DB 2; Length 1829;
Best Local Similarity 21.1%; Pred. No. 0.00011;
Matches 233; Conservative 157; Mismatches 469; Indels 245; Gaps 38;

```
Qy      2 EDIDQSSLVSSSTDSPPR-----PPPAFKYQFVTEPEDEE-----DEEEE-----E 42
      |:  ::| || : |      |      |||  ||      :  ||      |
Db      212 EETTVAVVESSGEEPASSSTSIPTELSKNDQVTEASGEETITAAATEASEETTTSAVTE 271

Qy      43 DEEEDDEDLEELEVLERKPAAGLSAAAVPPAAAAPLLDFFSSDSVPPAPRG---PLPAAPP 99
      ||  :  :|:  :||:  |:  ::|      :  ||  |      ||
Db      272 GSGEDTTVAVVVELSGEQPAS--SSTSIP-----TELSKDDQVTEASGEETTTAAATE 322

Qy     100 AAPERQPS-----WERSPAAPAPSLPPAAAVLPSKLPEDDE-PPARPPP 143
      |:  |      |      |      |||  |      :  :|:|  :||:  |
Db     323 ASEETTTSAVTEGSGEETTVAVVESSGEEPASS---STSIPTELSKDDQVTEASGEET 378

Qy     144 PPAGASPLAEPAPPPSTPAAPKRRGSGSVDETLFAL-----PAASEPVIPISSAEKIMD 196
      | |:  :|      | :      |||  | |:  |:      ||:|  ||:  |
Db     379 TTAAATEASE-----ETTTSAVTEGSGE-DTTVAVVESSGEQPASSSTSIPTELSKDDQ 432

Qy     197 LMEQPGN-----TVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEH 237
      :  |  |      |      ||:  ::      ::|:  :|  |  :
Db     433 VTEASGEETTTAAATEASEETTTSAVTEGSGEDTTVAVVESSGEQPASSSTSIPT---- 488

Qy     238 GYLGNL SAVSSSEGTI EETLINEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPK 297
      |      |:  :|  |||  |:  |  |  |  |      |:  :  :  :|  :
Db     489 -ELSKDDQVTEASG--EETTAAATEASEETTTSAVTEGSGEETTV-VAVVESSGEEPAS 544

Qy     298 GESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESPV-----GKEDRVVSPEKTM DI 350
      ::|  | :|:  :  :  :|  :|  | :|:  | :|  ||:  :  :|
Db     545 SSTSIPTELSKDDKVTEASGEETTTAAATDASSEETTTSAVTEGSGEETTVAVVESSD- 603

Qy     351 FNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLED SLEQ 410
      |  |  |  :  |  |  :  |  |  |  |  |  |  |  |  |  |  |
Db     604 -EEPASSSTSIPTELSKDDQVTEASGEETTT-----AAATEASEETTTSAVTEGSGEE 655

Qy     411 KSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKT 470
      ::  |  | :  :  ||  | :  |  :|  |  | :|||  :  | :  :
Db     656 TTVAVVESSGEEPASSSTSIPTELSKDDKVTEA--SGEETTTAAATDASSEETTTSAV 712

Qy     471 DEKKIEERKAQIITEKTSPK-TSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTP 529
      |  ||  :  :  :  | :  :  :|:  |  ||  :  :  |  ||  :  |
Db     713 TEGSGEETTVAVVESSDDEEPASSSTSIPTELSKDDQVTEASGEETTTAAATEASEETTT 772

Qy     530 DLVQEACESELN-----EATG-----TKIAYETKVDLVQTSEAIQESLYPTAQLCPSF 577
      |  |  |  | :|  |  |  |  |  |  |  |  |  |  |  :
Db     773 SAVTEGSGEETTVAVVESSGEEPASSSTSIPTELSKD-DQVTEASGEE---TTAAATE 828

Qy     578 EEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPY 637
      |  |  |  |  :  :  ::  |:  |  ||:  |  |  :|
Db     829 ASEETTTSAVTEGSGEDTTVAVVESSGE---QPASSSTSIPTELS----- 871

Qy     638 EEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFS NYSE 697
      |:  :  |:  :||  :  |  :  :||  |      :
```


Db 872 -----KDDQVTEASGEETTT---AAATEASEETTTSAVTEGSGEETTV 911

Qy 698 IAKFEKSVPEHAELVEDSSPESEPVDFLSDDSIPEV---PQTQEEAVMLMKESLTEVSET 754
 :| | | | | | | | | | :| | | :| | | | | :|

Db 912 VAVVLESSGEEPA-----SSSTSIPTELSKDDQVTEASGEETTTAAATEASSEETTTSAVT 966

Qy 755 VAQHKEERLSASPQELGKPYLESFQP-----NLHSTKDAASN----- 791
 :| | | :| :| | | :| :| :| :| :| :| :| :|

Db 967 EGSGEETTTSAVTEGSGEETTTSAVPEGENSTTEAPAFVTGSEIEIPSSSESSSTTTTHDP 1026

Qy 792 DIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESET-FSDSSPIEIIIDEFPTFVS 850
 || :| | :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 1027 SIPVITPKPSVSSSTIENVMSKTSSEE---AAEKKIIGEHQTKGDDDDAGKEDEDNMPAFVT 1083

Qy 851 A-----KDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCD 891
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 1084 ANPAGTSTTESAENVSTSTGEEDENIKMAKELGKQFAADLAKLA----- 1126

Qy 892 LSFKNIIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKK 951
 || | :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 1127 -----AKDGVNLT-ETADAKDSGETAHVEDEQVSSTE--SSIGSEETTTTVNKETTEE 1176

Qy 952 LPSDTEKEDRSLSAVLSAELSKTS 975
 :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 1177 HHEASGEEDDAPAFVTGAPTDSTT 1200

RESULT 11

A47282

calcium-binding protein calphotin - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

C;Accession: A47282

R;Martin, J.H.; Benzer, S.; Rudnicka, M.; Miller, C.A.

Proc. Natl. Acad. Sci. U.S.A. 90, 1531-1535, 1993

A;Title: Calphotin: a *Drosophila* photoreceptor cell calcium-binding protein.

A;Reference number: A47282; MUID:93165729; PMID:8094559

A;Accession: A47282

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-865 <MAR>

A;Cross-references: GB:L02111; NID:g157031; PIDN:AAA28405.1; PID:g157032

A;Experimental source: photoreceptor cells

A;Note: sequence extracted from NCBI backbone (NCBIN:124955, NCBIP:124956)

C;Genetics:

A;Gene: FlyBase:Cpn

A;Cross-references: FlyBase:FBgn0010218

C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; von Willebrand factor type C repeat homology

C;Keywords: calcium binding

Query Match 5.1%; Score 295.5; DB 2; Length 865;

Best Local Similarity 21.3%; Pred. No. 7.1e-05;

Matches 217; Conservative 127; Mismatches 379; Indels 295; Gaps 41;

Qy 62 AAGLSAAAVPPAAAAPLLDSSDSVPPAPRGPLPAAPPAAPER----QPSWERSPAAPAP 117
 :| :| | | | | :| :| | | :| :| :| :| :| :| :| :|

Db 11 SAPVAAPVTPSAVAAPVQVVSPAAPVAPAPAAPIAVTPVAPPPTLASVQPATVTIP-APAP 69

Qy 118 ----SLPPAAAVLPSKLPEDDEPPARPPPPPPAGA-----SPLAEPAAPSTP----- 161
|: | |: | : | | | | | |: | | | |

Db 70 IAAASVTPVASVAPPVVAAPTTPAASPSTPVAVAQIPVAVSAPVAPPVAATPTPVVQIP 129

Qy 162 -AAPKRRGSGSVDETLFALP--AASEP----VIPSSAEKIMDLMEQPGNT--VSSGQED 211
| | | : | | | | | | | : | | | |:

Db 130 VAAP-----VIATPPVAASAPTPAAVTPVISPVIASPPVVPANTTVPVAAPVAA 178

Qy 212 FPSVLLETAASL-PSLSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATN 270
|: : | | |::| | : : : | | | : |: | |

Db 179 VPAAPVVPVAPVLAPAVAPAVAPVVAETPAPPPVAEIPVA--TIPECVAPLIPEVSVVATK 236

Qy 271 PFVNRDLAEFSELEYSEMGSFSGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSP 330
| | | | | | | | | | | | | |

Db 237 PLA-----AAEPVVVAPPATETPVVAPAAASP 263

Qy 331 QESPVGKEDRVVSPEKTMDIFNEMQMSVAVPVREEYADFKPFEQAWEVKDTYEGSRDVLA 390
| | | | | : | | : : | | | |

Db 264 HVS-----VAP-----AVETA VVAPV----- 279

Qy 391 ARANVESKVDRKCLEDSEKSL---GKDSEGRNEDASFPSTPEPVKDSSRAYITCASF 446
|: | | | : | : | : | | | | : : : :

Db 280 -SASTEPPVAAATLTTPAPETPALAPVVAESQVAANTVVATPPTPAPEPETIAPPVVAETP 338

Qy 447 TSATESTTANTFPLEDHTSENKTDEKKIEERKAQIIITEKTSPKTSNPFLVAVQDSEADY 506
|: : | |:: : | | | | | | | | |:

Db 339 EVASVAVAETTPPVVPPVAAES-----IPAPVVATTVPVATLAVTDPD--- 381

Qy 507 VTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQES 566
| | : | | : | | | | | | | |

Db 382 -----VTASAVPELPPVIAPSPVPSA-----VAETPVDLA-----PPV 414

Qy 567 LYP-TAQLCPSF--EEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAP---- 619
| | | : | | | | | : : | | : : | | | |

Db 415 LPPVAAEPVPAVVAETPETPAPASAPVTI-AALD--IPEVAPVIAAPSDAPAEAPSAAA 471

Qy 620 PPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIACD-- 677
| | | | | | | | | | | | | | : : :

Db 472 PIVS-----TPPT-----TASVPETTAPPAAVPTEPI 498

Qy 678 ---LIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAE--LVEDSSPESEPVDLFSD-DSIP 731
: : | : | : | : | | | : | | | | |:

Db 499 DVSVLSEAAIETPVAPPVEVTTEVAVADVAPPEAAADLIEPVEPPAPIPDLLEQTTSPV 558

Qy 732 EVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQPNLHSTKDAASN 791
| : : : : | | : | | : : | : | | : |:

Db 559 AVEAAESTSSPIPETSLPPPNEAVA---SPEVAVAPITAPEPIPEP-EPSLATPTEPIPV 614

Qy 792 DIPTLTKKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIEIIDEFPTFVSA 851
: | : : | : : | : : | | | | |:

Db 615 EAPV-----VIQEAVDAVEVPVTETSTSIPETTVEFPEAVAE 651

Qy 852 KDDSPKLAKEYTDLEV-SDKSEIANIQSGAD---SLPCLEL-----PCDLSFKNIYP- 899
| | : | : : : | | | : | : | | : : | |

Db 652 KVLDPAI---TEAPVTTQEPDVANINDGAPATEITTPAVEIVTAAAEVSDIAIPVIDPP 707

```

Qy      900 -KDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMG----- 936
          |: |: | | : :: : | : | |:
Db      708 VPQEIAVA-EIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAAEVPITAGDN 766

Qy      937 ----SIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSSVVDLLYWRDIKKTGV 990
          |: |: : ||| : | | : : || ||: | |
Db      767 PDNTSVGISEVVPTIAEKPVEEVPTSEIPEQSSSPSDSVPAKITPLL--RDLQTTDV 822

```

RESULT 12

T34513

hypothetical protein ZK783.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T34513

R;Favello, A.; Vaudin, M.

submitted to the EMBL Data Library, August 1994

A;Description: The sequence of *C. elegans* cosmid ZK783.

A;Reference number: Z21536

A;Accession: T34513

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-3507 <FAV>

A;Cross-references: EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK783.1

A;Experimental source: strain Bristol N2; clone ZK783

C;Genetics:

A;Gene: CESP:ZK783.1

A;Map position: 3

A;Introns: 14/1; 48/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/2; 1450/1; 1760/1; 1898/1; 2153/1; 2628/1; 2681/1; 2899/1; 2946/1; 3088/3; 3184/1; 3283/1; 3346/3; 3365/3; 3484/3; 3504/1

Query Match 5.0%; Score 292; DB 2; Length 3507;

Best Local Similarity 20.6%; Pred. No. 0.00071;

Matches 226; Conservative 146; Mismatches 491; Indels 236; Gaps 37;

```

Qy      11 SSSTDSPRPPPAFKYQFVTEPEDEDEEEEEDEEDEDL--EELEVLERKPAAGLSAA 68
          |||:::| | : :|| : :|| | | : || | : |
Db      2043 SSSSEAPLTSSPATTTEVITESSVKSTTPKEESSSEITVKLSSKSPEVTESSVKSSPSTP 2102

Qy      69 AVPPAAAAPLLDFSSDSVPPAPRGPLPAAPP----AAPERQPSWERSPA-----APAPSL 119
          : : : :| | : :| : :| : :|| | : ||
Db      2103 STTSQSVTSTVPETSKSTVLSEAPVTSTSPTEVHTSSETKPSLSASSTTGDTNSTTPST 2162

Qy      120 PPAAAVLPSKLPEDDEPPARPPPPPPAGASP-LAEP-----AAPPSTPAAPKRRGSGSV 172
          |:| : || | | : ||::| | || | : ||
Db      2163 SSLASVKSTSAPEGTS--ASVAPVKLSSLSPDVSPSTKTFDATESSTVQASETSSGTSV 2220

Qy      173 DET-----LFALPAASEPVI-PSSAEKIMDLMEQPGNTVSSGQEDFP----SV 215
          | : :|| || | : : |||:| ||| | |
Db      2221 KSTSEPESHVTKLSITSSNPSSSVPTSPKSTPTVPESTEQPTSTTPSGQSLTPMNSNSE 2280

Qy      216 LLETA---ASLPSLSPLSTVSFKEHGYLGNLSAVSSSEGITIEETLNEASKELPERAT--N 270
          :| |: |||| : | | | : : :| :|| | | :
Db      2281 VLTTSEPHVLSSSLSPDVQSSTTPNNLSESSTVETPKTSSEVSLNSEEPSTTEAPTTL 2340

```

Qy	271	PFV-----NRDLAEFSEL---EYSEMGSSFKGSPKG-----ESAILVENTKEEVIVRSKD	317
Db	2341	PDILSTTTNNLSQSSTVSTEDRSEISSENSEKPTSAPELVTSVVTHVASSSPDVPTESS	2400
Qy	318	KEDLVCSAALHSPQ-----ESPVGKEDRVVSPEKTMDFNEMQMSVVAPVREEYADFK	370
Db	2401	PDDLTGSSSTENIPEASSKQTISSSTPTPDITTTASEEPTKSTSMSPDLSTTSNVLSSESSTTP	2460
Qy	371	PFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLEDLSLEQKSLGKDSEGRNEDASFPSTP	430
Db	2461	ESSSKSPVSSSTEG---ISVVTSTEFKSVPESTISSVLE-----EDLT-KTTP	2504
Qy	431	EPVKDSSRAYITCASFTSAT-----ESTTANTFPLEDHTSENKTDEKKIEE	477
Db	2505	SPILEET---TTASETSEPLTEDSLTVSVRIHELTTSSENVPKESSESTTSSESSKPSQ	2560
Qy	478	RKAQIIITEKTSPKTSPNPLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGL-----TPDLV	532
Db	2561	EPAGILTSTVVVPTSSVSLITASEIEA--ITSNTPFKQGRTPITTSKSLVKSTTSPSTV	2618
Qy	533	--QEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATSPVLPD	590
Db	2619	TSSEPSESTKRRTTVSTTVSTTTTPEETTTSESILITAAPSK--PTESTTESSEAPTP-	2674
Qy	591	IVMEAPLNSSLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGT	650
Db	2675	-----AKTSETKPS-----NVSSTSRKS	2692
Qy	651	KEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAE	710
Db	2693	TENVETSTSQSGSLESS-----TMSSTSSEPETNAPAVTVSSEASSTTLEE	2738
Qy	711	LVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKE-ERLSASPQE	769
Db	2739	NSSTSSPTSSEASVKLSSLFPE--SITSEAVTVSSRAPAEITMSSESHREISTVSSEPSE	2796
Qy	770	LGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSS-----	822
Db	2797	PEIPLSTTVSPNVVTASSIPSEE-PILSSVTSSSTPRVRLITG--TPDDLIVSVTVPSHG	2853
Qy	823	-KEDKIKESETFSDS-SPIEIIDFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGA	880
Db	2854	NRRQNITASSVPSNSTSPIILPSESLTPQPPPTTTTAKPAT-----TSGK	2900
Qy	881	DSLPCLELPCDLSFKNIYPKDEVHVSDEFSENRRSSVSKASISPSNVSALEPQTEMGSIKV	940
Db	2901	RGPPSIQPPAEM-----FTTPAPPPPSNGGYGEE-----	2929
Qy	941	SKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDDLlyWRDIKKTGVVFGASLFLLL	1000
Db	2930	----TNQEEEQVTSTTTTEAPSLCSTVTCHSLATCE-----QSTGVICICRDGFID	2976
Qy	1001	SLTVFSIVSVTAYIALALL	1019
Db	2977	GTTACSKKSTADCISLPSL	2995

A56577

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-Jul-1995 #sequence revision 21-Jul-1995 #text change 16-Feb-1997

C;Accession: A56577

R; Zauner, W.; Kratz, J.; Staunton, J.; Feick, P.; Wiche, G.

Eur. J. Cell Biol. 57, 66-74, 1992

A;Title: Identification of two distinct microtubule binding domains on recombinant rat MAP 1B.

A;Reference number: A56577; MUID:92347374; PMID:1639092

A;Accession: A56577

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-2364 <ZAU>

A; Cross-references: GB:X60550

A; Experimental source: brain

A;Note: nucleotide sequence not given; conceptual translation not complete

C;Superfamily: microtubule-associated protein MAP1B

Query Match 5.0%; Score 291.5; DB 2; Length 2364;
Best Local Similarity 20.0%; Pred. No. 0.00043;
Matches 220; Conservative 167; Mismatches 456; Indels 255; Gaps 44;

QY 30 TEPEDEEEEEEEEEDEEDEDLEELVLERKPAAGLSAAVPPAAAAAPLLDFSSDSVPPA 89
: | | | : | : | | : | : : | | | | : : | :
Db 913 S E E E G E E E E D K A E D A R E E D H E P D K T E - - - - - A E D Y V M A V D K A A E A G V T E D O Y D F L - - - 963

QY 90 PRGPLPAAPPAAPERQPSWERSPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPPPAGAS 149
 | : | : | | : | | |
 Db 964 -----GTPAKQ-----PGVQSPSREPASSIHDETLPGGSESEAT-----AS 999

Qy 150 PLAEPAAPSTPAAPKRRGSGSVDETLFAIPAASEPVIPSSAEKIMDLMEQPGN---TVS 206
 | | || | : :|| | :| | |
 Db 1000 DEENREDQPEEFTAT---SGYTQST---IEISSEPTPMDEMSTPRDVMTDETNNETES 1052

QY 207 SGQE-----DFPSVLLETAASLP---SLSPLS-----TVSFKEHGYLEGNLSAVSSSEGTIE 254
 || : || | | | : || | : | : |
 Db 1053 PSQEFVNITKYESSLYSQEYSKPVVASFNGLSDGSKTDATDGRDYNASASTISPPSSMEE 1112

```
Qy      255 ETLNEAS-----KELPERATNPFVNRDLAEF--SELEYSEMGG--- 289  
       :   :::  
Db     1113 DKFSKSALRDAYRPEETDVKTGAELDIKDVSERLSPAKSPSLSPSPSPSPIEKTPLGERS 1172
```

Yy 290 -----SSFKGSPKGESAILVENTKEEVIVR----SKDKEDL-----VCSAALHSP 330
: | | :||: :| : :| | :: | | :| ||:
Db 1173 VNFSLTPNEIKASAEGEATAVVSPGVTOAVVEEHCA SPEEKTLEVVSPOSVTGSAGHTP 1232

```

Qy      331 -QESPGVKEDRVVSPEKTMDFNEMQMSVVAPVREEYADFK-----PFEQAWEVKD 380
          :||  ::   :  ||           : :   ||  |: : |           | : :  ||
Db      1233 YYQSPTEKSSHLPT EVT-----ENAAQVPVSFEFTEAKDENERSSISPMDE--PVDP 1283

```

QY 381 TYEGSRDVLAAARANVESKVDKRCLED--SLEQKSLGKDS---EGRNEDASFPSTPEPVK 434
: ||: : || |: |:|: | ||: | ||
Db 1284 SESPIEKVLSPLRSPPLIGSESAYEDFLSADDKALGRRSESPFEGKNGKQGFSDKESPV 1343

Qy 435 DSSRAYITCASFTSATESTTANTFPLLEDHTSENKT-----DEKKI----- 475

```

      |   : |   :   |   |   | : | | : | |   | | : |
Db    1344 D-----LTSDLYQDKQEEKRAGFIPIKEDFSPEKKASDAEIMSSQSALALDERKLGGDGS 1398

Qy    476 -----EERKAQIIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAV-- 520
      | : | |   |   |   | : : |   : | :   | : : | : |
Db    1399 PTQVDVSQFGSKEDTKMSISEGTVSDKSATPVDEGAEDT---YSHMEGVASVSTASVAT 1455

Qy    521 SNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQES-LYPTAQLCP---S 576
      | : | | | | : : | : : | : | | | | : : | : : | |
Db    1456 SSFPEPTTDD-VSPSLHAEVGSPhSTEVDDSLSVSVVQTPTTFQETEMSPSKEECPRPMS 1514

Qy    577 FEEAEATP-----SPVLPDIVMEAPLNSLL-----PSAGASVVQ 610
      : : |   | : : | : | : | |   | : | | : :
Db    1515 ISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSLAMDFSRQSPDHPTVGAGMLH 1574

Qy    611 PSVSPLEAPPPVSYD-----SIKLEPENPPPYEEAMNVALKALGTKEGIKEPESFN 661
      : : | | | | | : | | | : : : : : : : | : :
Db    1575 ITEN---GPTEVDYSPSDIQDSSLHKIPPTTEEPSYTQDNDLS-ELISVSQVEASPSTSS 1630

Qy    662 AAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESEP 721
      |   | | | : : | | | | : : | : | | | : : | :
Db    1631 AHTPS-----QIASPLQEDTLSDVVPPrDMSLYASLASEKVQSLEGEKL----SPKSDI 1680

Qy    722 VDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYL-ESFQP 780
      | : | | : : | | | | : | : : : : | | : : |
Db    1681 SPLTPRESSPTYSPGFSdstSGAKES-TAAYQTSSSPIDAAAAEPYGRSSMLFDTMQH 1739

Qy    781 NLHSTKDAASNDIPTLTkKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE 840
      : | : : | : : : : : | : | | | : : : : | | :
Db    1740 HLALSRLTtSSV----EKDNGGKTPGDFNYAYQKPESTTESPDEEDYDYE--SHEKTIQ 1793

Qy    841 IIDEFPtFVSAKDDSPK----LAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKN 896
      | : : : : | : | : | : : | | | : : |
Db    1794 AHDVGGYYEYKERTERTIKSPCDSGSYETIEKTTKTP----EDGGYS-----CEITEKT 1842

Qy    897 IYPKDEVHVSDEFSENrSSVSKAS-----ISPSNVSALEPQTEMGSIVKSKSL 944
      : | | | | : : | : : : : : : : | : |
Db    1843 TRTPEEGGYSEISEKtTRTPEVSGYTYEKTERSRRLLDDISNGYDDTEDGGHTLGDCSY 1902

Qy    945 TKEAEKKLPSDTEKEDRS 962
      : | : | : | | |
Db    1903 SYETTEKITSPPESESYS 1920

```

RESULT 14

T19431

hypothetical protein C25A1.10 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C;Accession: T19431

R;Mortimore, B.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19124

A;Accession: T19431

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-971 <WIL>

A;Cross-references: EMBL:Z81038; PIDN:CAB02755.1; GSPDB:GN00019; CESP:C25A1.10
A;Experimental source: clone C25A1
C;Genetics:
A;Gene: CESP:C25A1.10
A;Map position: 1
A;Introns: 38/3; 92/3; 201/3; 919/3
C;Superfamily: nucleolus-cytoplasm shuttle phosphoprotein

Query Match 4.9%; Score 288.5; DB 2; Length 971;
Best Local Similarity 20.6%; Pred. No. 0.00016;
Matches 198; Conservative 127; Mismatches 391; Indels 247; Gaps 35;

```

Qy      7 SSLVSSSTDSPRPPPAFKYQFVTEP---EDEEDEEEEEDEEEDDEDLEELEVLERKPAA 63
      || || || ||: || : : | : : : : : | : || : : : | |
Db     147 SSSDSDSDDEPPKKAPAVTTKVAPKPMAKKQDTSDDSDSDSESDDDGKSKKANPVKVTPVA 206

Qy     64 GLSAAAVPPAAAPLLDFSSDSVPPAPRGPLPAAPPAAP-----ERQPSWE 109
      : | | | | : | | | | : | | | | | | | | | | : | : |
Db     207 NVLQKVVAKKAASSSDSDDEKKPAAK-PTPAKPTPKPVVKAESSSDSDDEKKPVAK 265

Qy    110 RSPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAAPPSTPAAPKRRGS 169
      : || | | | | | | | | | | | | | | | | | | | : : :
Db    266 PPAKATPK-PAKKADSSSDSSDDEAPAK-KTPAKAAPKPVAKKAESSSDSDDEKK-- 321

Qy    170 GSVDETLFAALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPL 229
      || | | | : | : : : | : | : : | : : | :
Db    322 -----PAAK-----PTPAKATPKPVAKKAESSSDSDDEKKPVAKPAPAKATPKPV 367

Qy    230 STVSFKEHGYLGNL SAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSE-- 287
      : | | | : : : | : | | : | | | : | : | : |
Db    368 AK-----KAESSSDSDDEK-KPAAKPTPAKATPKPVAKKAESSSDSDDEKK 414

Qy    288 ---MGSSFKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSP 344
      : | | : | | : | | | : | | | : | | | : |
Db    415 PVAKPTSATPK-----PAKKAD---SSSDSSDDEAPAKKTPAKAAP 455

Qy    345 E---KTMDIFNEMQMSVAPVREEYADFKPFEQAWEVKDTYEGSRD-----VLAARANV 395
      : | | : : : : | | | | : | | : | | | | |
Db    456 KPASKKAESSSDSDDEKPAAKSTPAKITPKPTAKKVASSSDSDDEKKPAAKPTPANA 515

Qy    396 ESKVDRKCLEDL-----EQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSAT 450
      | | | | | : | : | : : : : | | : : : :
Db    516 TPKPVAKKAESSSDSDDEKKPVAKPTSAK-----ATPKPAKKADLSSDFSDDEAPA 568

Qy    451 ESTTANTFPLEDHTSENKTDEKKIEERKAQIIITEKTSFK-TSNPFLVAVQDSEADYVTT 509
      : | | | : : : | : | : | | | | : : | | |
Db    569 KKTPAKAAPKPAKKAESSSDSDDEKPAAKSTPAKTTPKPTAKKAASSSDSDSD--EK 626

Qy    510 DTLKSVTEAAVSNMPEGLTPDLVQEACESELN-----EATGTKIAYETKVDLVQTSEAI 563
      : : | | | : | | : : : | : | | : | | | : : :
Db    627 KPVAKPTSATPKPAKKADSSSDSDDEAPAKKTPVKPTPVKIVAK-KVD--SSSDSS 683

Qy    564 QESLYPTAQLCPSFEEAEATPSVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVS 623
      : || | : | | | | | | : | | | |
Db    684 DDEKKPT-----KATPVKVTP-----KSVTKKAAAS-----S 710

Qy    624 YDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIIACDLIKETK 683

```

Db	711	SDS--SDDEKKPVVKQTPNVV-----PKKEKAASSSDSS-----DDEKK	748
Qy	684	LSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESEPVDFLSDDSIPEVPQTQEEAVML	743
Db	749	PTAKPTP-----KATPKQSAKKADSSDDS-----SDDEAPA-----	779
Qy	744	MKESLTEVSETVAQHKEERLSASPQELGKPYLESFQPNLHSTKDAASNDIPTLTKEKIS	803
Db	780	-----KKTPAKSTPAKTAVKKEASS	799
Qy	804	LQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDS--PKLAKE	861
Db	800	-----SSDDSSDDEKTKKKSATTPAKSTPKTALKKAESSDSSDDDEDLPKPSKA	848
Qy	862	YTDL-EVSDKSEIANIQSGADSLPCLEL-PCDLSFKNIYPKDEVHVSDEFSENRSSVSKA	919
Db	849	VTPRPQRADSEESAETEESSSRTPALKAKPLATSTEKAVYENRKRKSSPF--RRVQMTKD	906
Qy	920	SIS	922
Db	907	SVS	909

RESULT 15

QRMSPI

microtubule-associated protein MAP1B - mouse

N;Alternate names: microtubule-associated protein MAP1(X); microtubule-associated protein MAP1.2; microtubule-associated protein MAP5

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 01-Sep-2000

C;Accession: S07549; S44387; A33645

R;Noble, M.; Lewis, S.A.; Cowan, N.J.

J. Cell Biol. 109, 3367-3376, 1989

A;Title: The microtubule binding domain of microtubule-associated protein MAP1B contains a repeated sequence motif unrelated to that of MAP2 and tau.

A;Reference number: A33645; MUID:90094539; PMID:2480963

A;Accession: S07549

A;Molecule type: mRNA

A;Residues: 1-2464 <NOB>

A;Cross-references: EMBL:X51396; NID:g52999; PIDN:CAA35761.1; PID:g53000

R;Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.

Arch. Biochem. Biophys. 310, 428-432, 1994

A;Title: Binding of heat-shock protein 70 (hsp70) to tubulin.

A;Reference number: S44387; MUID:94234720; PMID:8179328

A;Accession: S44387

A;Status: preliminary

A;Molecule type: protein

A;Residues: 653-663, 'IC' <SAN>

C;Superfamily: microtubule-associated protein MAP1B

C;Keywords: microtubule binding; phosphoprotein; tandem repeat

F;589-786/Domain: microtubule binding #status experimental <MTB>

F;589-592,639-642,649-652,655-658,660-663,668-671,674-677,679-682,683-686,687-

690,691-694,695-698,699-702,708-711,712-715,716-719,720-723,727-730,758-761,764-

767,783-786/Region: 4-residue repeats (K/R-K-E/D-X)

F;1861-2064/Region: 17-residue repeats

F;91,116,351,888,1124,1153,1168,1208,1662,1877,1918,2003,2030,2054,2083/Binding site: phosphate (Ser) (covalent) #status predicted
F;147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (covalent) #status predicted
F;1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 4.9%; Score 284; DB 1; Length 2464;
Best Local Similarity 20.7%; Pred. No. 0.00092;
Matches 233; Conservative 159; Mismatches 424; Indels 312; Gaps 51;

```
Qy      31 EPEDEEDEEEEEDEED-----DEDLEELE-----VLERKPAAG-----LSAAAVP 71
      | | :| |||: | | : | | | :| :| | | :|
Db    1009 EAEQSEEEGEEEDKAEDAREEGYEPDKTEADYVMAVADKAAEAGVTEEQYGYLGTSKQ 1068

Qy      72 PAAAAPLLDFFS---DSVPPAPRGPLPAAPPAAPERQP-----SWERSPAAPA 116
      | :| : :| :| :| :| :| :| :| :| :|
Db    1069 PGIQSPSREPASSIHDETLPGGSESEATASDEENREDQPEEFTATSGYTQSTIEISSEPT 1128

Qy     117 P---SLPPAAVLPSKLPEDDEPPARP-----PPPPPAGASPLAEP-- 155
      | | : | :| :| :| :| :| :| :| :| :|
Db    1129 PMDEMSTPRDVMSDETNNETESPSQEFVNITKYESSLYSQEYSKPAVASFNGLSEGSKT 1188

Qy     156 -----APPSTPAAPKRRGSGSVDETLFALPA-----ASEPVIPSSAEKIMDLMEQ 200
      | | : | :| :| :| :| :| :| :| :| :|
Db    1189 DATDGKDYNASASTISPP-----SSMEEDKFKSKALRDAYCSEEKELKASAE--LDIKDV 1241

Qy     201 PGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLGNL SAVSSSEG TIEETLNEA 260
      :| | | | | | | | | | | | | | | |
Db    1242 SDERLS-----PAKSPSLSP-----SPPSPIEKT---- 1265

Qy     261 SKELPERATNPFVNRDLAEFS----ELEYSEMGSFSGSPKGESAILVEN--TKEEVIVR 314
      | ||: | | | | :| :| :| :| :| :| :| :|
Db    1266 --PLGERSVN-----FSLTPNEIKVSAEGEARSVSPGVTQAVVEEHCASPEEKTLE 1314

Qy     315 SKDKEDLVCSAALHSP--QESPVGKEDRVVSPEKTMDIFNEMQMSVVA--PVREEYADFK-- 370
      :| :| :| :| :| :| :| :| :| :| :| :|
Db    1315 VVSPSQSVTGSAGHTPYQSP-----TDEKSSHLPTVSENAQAVPVSFSEAKDE 1366

Qy     371 -----PFEQAWEVKDTYEGSRDVLAAARANVESKVDRCLED--SLEQKSLGKDS---- 417
      | :| :| :| :| :| :| :| :| :| :| :|
Db    1367 NERASLSPMDE--PVPDSESPVEKVLSPLRSPPLLGSESPYEDFLSADSKVLGRRESPEF 1424

Qy     418 EGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLEDHTSENKT----- 470
      ||:| || || : : : : : : : : : | | |
Db    1425 EGKNGKQGFPDRESPVSDLT----STGLYQDKQEEKSTGFIPIKEDFGPEKKTSDVETMS 1480

Qy     471 -----DEKKI-----EERKAQII TEKTS PKTSNPF L VAVQDSEAD 505
      ||:| :| :| :| :| :| :| :| :| :|
Db    1481 SQSALALDERKLGGDVSPTQIDVSQFGSFKEDTKMSISEGTVSDKSATPVDEGV--AEDT 1538

Qy     506 YVTTDTLSKVTEAAV--SNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAI 563
      | : :| :| :| :| :| :| :| :| :| :|
Db    1539 YSHMEGVASVSTASVATSSFPEPTDD--VSPSLHAEVGS PHSTEVDDSLSVSVVQTPTTF 1597

Qy     564 QES-LYPTAQLCP---SFEEAEATP-----SPVLPDIMEAPLNSLL-- 601
      ||: :| :| :| :| :| :| :| :| :| :|
Db    1598 QETEMSPSKEECPRPMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSFAMD 1657
```

Qy 602 -----PSAGASVVQPSVSPLEAPPPVSYD-----SIKLEPENPPPYEEAMNVA 644
 Db 1658 FSRQSPDHPTLGASVLHITEN---GPTEVDYSPCDIQDSSLSHKIPPTTEEPSYTDNDLS 1714

Qy 645 LKALGTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDFSNYSEIAKFEKS 704
 Db 1715 -ELISVSQVEASPSTSSAHTPS-----QIASPLQEDTLSDVVPREMSLYASLA----- 1762

Qy 705 VPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVML---MKESLTEVSETVAQHKE 760
 Db 1763 ----SEKVQ--SLEGEKLSPKSDIS----PLTPRESSPLYSPGFSDDSTSAKETAAAH-- 1810

Qy 761 ERLSASP---QELGKPY-----LESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFN 810
 Db 1811 -QASSPPIDAATAEPYGFSSMLFDTMQHHLALNRDLTTSSV---EKDSGGKTPGDFN 1865

Qy 811 TAIYSNDDLSSKEDKIKESETFSDDSPIEIIDFPPTFVSAKDDSPK---LAKEYTDLE 866
 Db 1866 YAYQKPENAAGSPDEEDYDYE--SQEKTIRTHDVVRYYYEKTERTIKSPCDSGYSYETIE 1923

Qy 867 VSDKSEIANIQSGADSLPCLLPCDLSPKNIYPKDEVHVSDEFSENRSSVSKAS----- 920
 Db 1924 KTTKTP---EDGG-----YTCEITEKTTTRTPEEGGYSYEISEKTTTRTPEVSGYTYEK 1972

Qy 921 -----ISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRS 962
 Db 1973 TERSRRLDDISNGYDDTEDGGHTLGDCSYSYETTEKITSFPESESYS 2020

Search completed: December 19, 2003, 15:37:23
 Job time : 34 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2003, 15:29:47 ; Search time 18 Seconds
 (without alignments)
 3038.448 Million cell updates/sec

Title: US-09-830-972-2
 Perfect score: 5848
 Sequence: 1 MEDIDQSSLVSSSTDSPRP.....VKDAMAKIQAKIPGLKRKAD 1163

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	5848	100.0	1163	1	RTN4_RAT	Q9jk11	rattus norv
2	4403.5	75.3	1192	1	RTN4_HUMAN	Q9nqc3	homo sapien
3	917	15.7	199	1	RTN4_MOUSE	Q99p72	mus musculu
4	801	13.7	777	1	RTN1_RAT	Q64548	rattus norv
5	789.5	13.5	776	1	RTN1_HUMAN	Q16799	homo sapien
6	625.5	10.7	236	1	RTN3_HUMAN	O95197	homo sapien
7	625.5	10.7	237	1	RTN3_MOUSE	Q9es97	mus musculu
8	509	8.7	471	1	RTN2_MOUSE	O70622	mus musculu
9	490	8.4	545	1	RTN2_HUMAN	O75298	homo sapien
10	308.5	5.3	5147	1	PCLO_HUMAN	Q9y6v0	homo sapien
11	300	5.1	5120	1	PCLO_CHICK	Q9pu36	gallus gall
12	295.5	5.1	865	1	CPN_DROME	Q02910	drosophila
13	291.5	5.0	2459	1	MAPB_RAT	P15205	rattus norv
14	288	4.9	2468	1	MAPB_HUMAN	P46821	homo sapien
15	284	4.9	2464	1	MAPB_MOUSE	P14873	mus musculu
16	282.5	4.8	2805	1	MAPA_HUMAN	P78559	homo sapien
17	279	4.8	5038	1	PCLO_MOUSE	Q9qyx7	mus musculu
18	275.5	4.7	3924	1	ANK2_HUMAN	Q01484	homo sapien
19	275	4.7	1972	1	P531_HUMAN	Q12888	homo sapien
20	272	4.7	5085	1	PCLO_RAT	Q9jks6	rattus norv
21	267	4.6	1781	1	AK12_HUMAN	Q02952	homo sapien
22	265.5	4.5	1828	1	MAP2_MOUSE	P20357	mus musculu
23	261.5	4.5	1087	1	NFH_MOUSE	P19246	mus musculu
24	259.5	4.4	1020	1	NFH_HUMAN	P12036	homo sapien
25	259.5	4.4	2404	1	SON_MOUSE	Q9qx47	mus musculu
26	258.5	4.4	1861	1	MAP2_RAT	P15146	rattus norv
27	257.5	4.4	2715	1	TRX2_HUMAN	Q9umn6	homo sapien
28	256	4.4	1723	1	AIM1_HUMAN	Q9y4k1	homo sapien
29	255.5	4.4	1140	1	YM96_YEAST	Q04893	saccharomyc
30	254.5	4.4	6632	1	UN89_CAEEL	O01761	caenorhabdi
31	254	4.3	1616	1	P200_MYCCE	Q49429	mycoplasma
32	254	4.3	3381	1	PGCV_BOVIN	P81282	bos taurus
33	253	4.3	3421	1	TEGU_HSVB	P28955	equine herp
34	252.5	4.3	1411	1	TCOF_HUMAN	Q13428	homo sapien
35	252	4.3	2738	1	PGCV_RAT	Q9erb4	rattus norv
36	250.5	4.3	4377	1	ANK3_HUMAN	Q12955	homo sapien
37	248.5	4.2	1189	1	YJH6_YEAST	P47035	saccharomyc
38	248	4.2	1827	1	MAP2_HUMAN	P11137	homo sapien
39	245.5	4.2	1001	1	IF2_SYNY3	P72689	synechocyst
40	244	4.2	1338	1	ACIN_MOUSE	Q9jix8	mus musculu
41	241.5	4.1	8545	1	ANC1_CAEEL	Q9n4m4	caenorhabdi
42	238.5	4.1	831	1	NFH_RAT	P16884	rattus norv

43	238.5	4.1	1341	1	ACIN_HUMAN	Q9ukv3 homo sapien
44	238	4.1	1306	1	MSB2_YEAST	P32334 saccharomyc
45	236.5	4.0	2774	1	MAPA_RAT	P34926 rattus norv

ALIGNMENTS

RESULT 1

RTN4_RAT

ID RTN4_RAT STANDARD; PRT; 1163 AA.

AC Q9JK11; Q9JK10; Q9R0D9; Q9WUE9; Q9WUF0;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)

DE (Glut4 vesicle 20 kDa protein).

GN RTN4 OR NOGO.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.

RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;

RX MEDLINE=99249816; PubMed=10231557;

RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;

RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:

RT a new member of the reticulon family.";

RL Biochim. Biophys. Acta 1450:68-76(1999).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

RX MEDLINE=20129258; PubMed=10667796;

RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,

RA Spillmann A.A., Christ F., Schwab M.E.;

RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an

RT antigen for monoclonal antibody IN-1.";

RL Nature 403:434-439(2000).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).

RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;

RA Ito T., Schwartz S.M.;

RT "Cloning of a member of the reticulon gene family in rat: one of two

RT minor splice variants.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP FUNCTION.

RX MEDLINE=22033691; PubMed=12037567;

RA GrandPre T., Li S., Strittmatter S.M.;

RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";

RL Nature 417:547-551(2002).

CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help

CC block the regeneration of the nervous central system in adults (By

CC similarity).

CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By

CC similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the

CC membrane of the endoplasmic reticulum through 2 putative
 CC transmembrane domains (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=Nogo-A, NI-220-250;
 CC IsoId=Q9JK11-1; Sequence=Displayed;
 CC Name=2; Synonyms=Nogo-B, Foocen-M1;
 CC IsoId=Q9JK11-2; Sequence=VSP_005658;
 CC Name=3; Synonyms=Nogo-C, VP20;
 CC IsoId=Q9JK11-3; Sequence=VSP_005656, VSP_005657;
 CC Name=4; Synonyms=Foocen-M2;
 CC IsoId=Q9JK11-4; Sequence=VSP_005659;
 CC -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic
 CC nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
 CC present in dorsal root ganglion, sciatic nerve and PC12 cells
 CC after longer exposure. Isoforms 2 and 3 are detected in kidney,
 CC cartilage, skin, lung and spleen. Isoform 3 is expressed at high
 CC level in skeletal muscle. In adult animals isoform 1 is expressed
 CC mainly in the nervous system.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF051335; AAF01564.1; -.
 DR EMBL; AJ242961; CAB71027.1; -.
 DR EMBL; AJ242962; CAB71028.1; -.
 DR EMBL; AJ242963; CAB71029.1; -.
 DR EMBL; AF132045; AAD31019.1; -.
 DR EMBL; AF132046; AAD31020.1; -.
 DR GO; GO:0030176; C:endoplasmic reticulum membrane, intrinsic p. . . ; IDA.
 DR GO; GO:0005635; C:nuclear membrane; ISS.
 DR GO; GO:0005515; F:protein binding activity; ISS.
 DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
 DR GO; GO:0030517; P:negative regulation of axon extension; ISS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT DOMAIN 1 989 CYTOPLASMIC (Potential).
 FT TRANSMEM 990 1010 POTENTIAL.
 FT DOMAIN 1011 1104 LUMENAL (Potential).
 FT TRANSMEM 1105 1125 POTENTIAL.
 FT DOMAIN 1126 1163 CYTOPLASMIC (Potential).
 FT DOMAIN 976 1163 RETICULON.
 FT DOMAIN 33 46 POLY-GLU.
 FT DOMAIN 73 76 POLY-ALA.
 FT DOMAIN 140 145 POLY-PRO.
 FT VARSPLIC 1 964 Missing (in isoform 3).
 FT /FTId=VSP_005656.
 FT VARSPLIC 965 975 AVLSAELSKTS -> MDGQKKHWKDK (in isoform
 FT 3).

Db	661	NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Qy	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Db	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Qy	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Db	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Qy	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Db	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Qy	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSI VKSKSLTKEAEKKLPDTEKED	960
Db	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSI VKSKSLTKEAEKKLPDTEKED	960
Qy	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Db	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Qy	1021	VTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Db	1021	VTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Qy	1081	FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA	1140
Db	1081	FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA	1140
Qy	1141	NKSVKDAMAKIQAKIPGLKRKAD	1163
Db	1141	NKSVKDAMAKIQAKIPGLKRKAD	1163

RESULT 2

RTN4_HUMAN

ID RTN4_HUMAN STANDARD; PRT; 1192 AA.
 AC Q9NQC3; Q94962; Q9BXG5; Q9H212; Q9H3I3; Q9UQ42; Q9Y293; Q9Y2Y7;
 AC Q9Y5U6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
 DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific
 DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
 GN RTN4 OR NOGO OR ASY OR KIAA0886.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=20129242; PubMed=10667780;
 RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,
 RA Michalovich D., Simmons D.L., Walsh F.S.;

RT "Inhibitor of neurite outgrowth in humans.";
 RL Nature 403:383-384(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RX MEDLINE=21010696; PubMed=11126360;
 RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
 RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
 RT endoplasmic reticulum and reduces their anti-apoptotic activity.";
 RL Oncogene 19:5736-5746(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=20237542; PubMed=10773680;
 RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;
 RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome
 RT 2p14-->2p13 by radiation hybrid mapping.";
 RL Cytogenet. Cell Genet. 88:101-102(2000).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RA Jin W.-L., Ju G.;
 RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=Placenta, and Skeletal muscle;
 RA Ito T., Schwartz S.M.;
 RT "Cloning of a member of the reticulon gene family in human.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Fibroblast;
 RA Yutsudo M.;
 RT "Isolation of a cell death-inducing gene.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Pituitary;
 RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
 RA Luo B., Hu R., Chen J.;
 RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RT "Novel human cDNA clone with function of inhibiting cancer cell
 RT growth.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=99156230; PubMed=10048485;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XII.
 RT The complete sequences of 100 new cDNA clones from brain which code

RT for large proteins in vitro.";
 RL DNA Res. 5:355-364(1998).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=Brain, Pancreas, Placenta, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=20499367; PubMed=11042152;
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
 RT "Cloning and functional analysis of cDNAs with open reading frames for
 RT 300 previously undefined genes expressed in CD34+ hematopoietic
 RT stem/progenitor cells.";
 RL Genome Res. 10:1546-1560(2000).
 RN [12]
 RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
 RC TISSUE=Brain;
 RA Mao Y.M., Xie Y., Zheng Z.H.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
 RN [13]
 RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RA Sha J.H., Zhou Z.M., Li J.M.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [14]
 RP TOPOLOGY.
 RC TISSUE=Brain;
 RX MEDLINE=20129259; PubMed=10667797;
 RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;
 RT "Identification of the Nogo inhibitor of axon regeneration as a
 RT Reticulon protein.";
 RL Nature 403:439-444(2000).
 RN [15]
 RP FUNCTION.
 RC TISSUE=Brain;

RX MEDLINE=21069055; PubMed=11201742;
 RA Fournier A.E., Grandpre T., Strittmatter S.M.;
 RT "Identification of a receptor mediating Nogo-66 inhibition of axonal
 RT regeneration.";
 RL Nature 409:341-346(2001).
 RN [16]
 RP REVIEW.
 RX MEDLINE=21888956; PubMed=11891768;
 RA Ng C.E.L., Tang B.L.;
 RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
 RT regeneration.";
 RL J. Neurosci. Res. 67:559-565(2002).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults.
 CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.
 CC This is likely consecutive to their change in subcellular
 CC location, from the mitochondria to the endoplasmic reticulum,
 CC after binding and sequestration.
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum. Anchored to the membrane of the endoplasmic reticulum
 CC through 2 putative transmembrane domains.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;
 CC IsoId=Q9NQC3-1; Sequence=Displayed;
 CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;
 CC IsoId=Q9NQC3-2; Sequence=VSP_005655;
 CC Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
 CC IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
 CC Name=4;
 CC IsoId=Q9NQC3-4; Sequence=VSP_005654;
 CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
 CC and testis and weakly in heart and skeletal muscle. Isoform 2 is
 CC widely expressed excepted for the liver. Isoform 3 is expressed in
 CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-
 CC specific.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -!- CAUTION: Ref.11 sequence differs from that shown due to
 CC frameshifts in positions 1149 and 1156.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AJ251383; CAB99248.1; -.
 DR EMBL; AJ251384; CAB99249.1; -.
 DR EMBL; AJ251385; CAB99250.1; -.
 DR EMBL; AB040462; BAB18927.1; -.
 DR EMBL; AB040463; BAB18928.1; -.
 DR EMBL; AF148537; AAG12176.1; -.
 DR EMBL; AF148538; AAG12177.1; -.
 DR EMBL; AF087901; AAG12205.1; -.

DR EMBL; AF320999; AAG40878.1; -.
 DR EMBL; AF132047; AAD31021.1; -.
 DR EMBL; AF132048; AAD31022.1; -.
 DR EMBL; AB015639; BAA83712.1; -.
 DR EMBL; AF077050; AAD27783.1; -.
 DR EMBL; AF177332; AAG17976.1; -.
 DR EMBL; AB020693; BAA74909.1; -.
 DR EMBL; BC001035; AAH01035.1; -.
 DR EMBL; BC007109; AAH07109.1; -.
 DR EMBL; BC014366; AAH14366.1; -.

Query Match 75.3%; Score 4403.5; DB 1; Length 1192;
 Best Local Similarity 75.9%; Pred. No. 3e-159;
 Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;

Qy 1 MEDIDQSSLVSSSTDSPRRPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEELEVLERK 60
 |||:|||| ||||| ||||| ||||| ||||| |||||:|::| ||||| |||||
 Db 1 MEDLDQSPLVSSS-DSPPRPQAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK 58

Qy 61 PAAGLSAAAVP--PAAAAPLLDFFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
 ||||| || ||| |||:| | ||||| ||||| |||||:| | : |
 Db 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSSTVP 118

Qy 116 APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
 ||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178

Qy 167 RG-SGSVDETLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
 || ||||| ||||| ||||| ||||| ||||| |||||:|:| ||||| ||||| |||||
 Db 179 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237

Qy 226 LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285
 ||||| ||||| ||||| | :|||:| :|||:| :| :| :||| |||||
 Db 238 LSPLSAAASFKEHEYLGNLSTVLPTETLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297

Qy 286 SEMGSSFFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339
 ||||| ||| |||:| | :||:|:|:|:|:| | : ||: || | |||
 Db 298 SEMGSSFSVSPKAESAVIVANPREEIVKNKDEEEKLVSNILHNQQELPTALTKLVKED 357

Qy 340 RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAWVEVKDITYEGSRDVLAA----RANV 395
 ||| || | ||| :| | :||| |||||: ||||: | | :||| :|:
 Db 358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy 396 ESKVDRKCLEDLSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
 |||||:| ||||| : |||| | :| ||||| :| | ||||| | :|||
 Db 417 ESKVDKCKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAAATESIA 476

Qy 455 ANTFLLEDHTSENKTDEKKIEERKAQIIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
 | |||| | ||||| |||||:|||:||| || ||||| ||||| ||||| |:
 Db 477 TNIFPLLGDPTSENKTDEKKIEEKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 536

Qy 514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTGKIAYETKVDLVQTSEAIQESLYPTAQL 573
 |||| |:||||| ||||| ||||| ||||| ||||| ||||| :||| |||||
 Db 537 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTGKIAYETKMDLVQTSEVMQESLYPAAQL 596

Qy 574 CPSFEEAEATPSPVLPDI VMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPEN 633
 |||||:||||| ||||| ||||| :|||:| ||||| | :|:| |||||

RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE OF 170-199 FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults (By
 CC similarity).
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
 CC membrane of the endoplasmic reticulum through 2 putative
 CC transmembrane domains (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=A number of isoforms may be produced;
 CC Name=1;
 CC IsoId=Q99P72-1; Sequence=Displayed;
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF326337; AAK08076.1; -.
 DR EMBL; AK003859; -; NOT_ANNOTATED_CDS.
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0030176; C:endoplasmic reticulum membrane, intrinsic p. . .; ISS.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0005635; C:nuclear membrane; ISS.
 DR GO; GO:0005515; F:protein binding activity; ISS.
 DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
 DR GO; GO:0030517; P:negative regulation of axon extension; ISS.

```

DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
KW      Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT      DOMAIN          1          25          CYTOPLASMIC (Potential).
FT      TRANSMEM        26          50          POTENTIAL.
FT      DOMAIN          51         137          LUMENAL (Potential).
FT      TRANSMEM        138         162          POTENTIAL.
FT      DOMAIN          163         199          CYTOPLASMIC (Potential).
FT      DOMAIN          12         199          RETICULON.
SQ      SEQUENCE        199 AA;  22466 MW;  07BE5D580059ED9C CRC64;

```

RESULT 4

```

CC  -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM MEMBRANE (BY
CC  SIMILARITY).
CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=RTN1-B; Synonyms=S-RexB;
CC      IsoId=Q64548-1; Sequence=Displayed;
CC      Name=RTN1-S; Synonyms=S-RexS;
CC      IsoId=Q64548-2; Sequence=VSP_005647, VSP_005648;
CC  -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CENTRAL AND
CC  PERIPHERAL NERVOUS SYSTEM OF NEWBORN AND ADULT RATS. LOW LEVELS
CC  HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.
CC  EXPRESSION OF ISOFORM RTN1-B IS RESTRICTED TO PARTICULAR NEURONAL
CC  TYPES.
CC  -!- DEVELOPMENTAL STAGE: DETECTED ON EMBRYONIC DAY E10 IN THE
CC  HINDBRAIN AND IN E11 IN THE FOREBRAIN. DURING THE NEXT 3 EMBRYONIC
CC  DAYS THE LEVELS OF S-REXS INCREASES AND REMAINS STABLE AT E13 IN
CC  THE HINDBRAIN AND AT E14 IN THE FOREBRAIN. THE LEVELS OF S-REXB
CC  DOES NOT CHANGE AS SIGNIFICANTLY DURING DEVELOPMENT OF THE
CC  HINDBRAIN.
CC  -!- SIMILARITY: Contains 1 reticulon domain.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; U17604; AAC53046.1; -.
DR  EMBL; U17603; AAC53045.1; -.
DR  InterPro; IPR003388; Reticulon.
DR  Pfam; PF02453; Reticulon; 1.
DR  PROSITE; PS50845; RETICULON; 1.
KW  Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT  TRANSMEM      604      624      POTENTIAL.
FT  TRANSMEM      727      747      POTENTIAL.
FT  DOMAIN        590      777      RETICULON.
FT  DOMAIN        610      613      POLY-LEU.
FT  VARSPLIC       1      569      Missing (in isoform RTN1-S).
FT                                     /FTId=VSP_005647.
FT  VARSPLIC      570      589      IPGPLGSDLVPPLPFFNKQK -> MQATADSTKMDCVWSNW
FT                                     KSQ (in isoform RTN1-S).
FT                                     /FTId=VSP_005648.
SQ  SEQUENCE      777 AA;  83001 MW;  AF7479C50F28D0AC CRC64;

```

```

Query Match          13.7%;  Score 801;  DB 1;  Length 777;
Best Local Similarity 32.4%;  Pred. No. 1.5e-23;
Matches 258;  Conservative 109;  Mismatches 264;  Indels 166;  Gaps 32;

```

```

QY      485 EKTSPKTSNPFLVAVQDSE-----ADYVTTDTL----SKVTEAAVSNMPEGL--TPD 530
      |: :|| : | | || | | | | | | | | | | | | | | | | | | | | | | |
Db      29 EEATPKGARP---AQQDGEPAWGSGAGAGVVSSRGLCSGPARSPPVAMETASTGVAAVPD 85

QY      531 LVQEACESELNEATG-----TKIAYETKVDLVQTSEAIQ-ESLYPTAQLCPSFEEAEA 582
      : : | : | | | | | | | | | | | | | | | | | | | | | | | |
Db      86 ALDHSSSPTLKDGEACYSLSIDICYPRED SAYFTGILQKENGHITTSESP---EELG 142

```


DE Reticulon 1 (Neuroendocrine-specific protein).
 GN RTN1 OR NSP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS RTN1-A; RTN1-B AND RTN1-C).
 RC TISSUE=Lung carcinoma;
 RX MEDLINE=93293865; PubMed=7685762;
 RA Roebroek A.J.M., Van de Velde H.J.K., Van Bokhoven A., Broers J.L.V.,
 RA Ramaekers F.C.S., Van de Ven W.J.M.;
 RT "Cloning and expression of alternative transcripts of a novel
 RT neuroendocrine-specific gene and identification of its 135-kDa
 RT translational product.";
 RL J. Biol. Chem. 268:13439-13447(1993).
 RN [2]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=96429995; PubMed=8833145;
 RA Roebroek A.J.M., Ayoubi T.A.Y., Van de Velde H.J.K.,
 RA Schoenmakers E.F.P.M., Pauli I.G.L., Van de Ven W.J.M.;
 RT "Genomic organization of the human NSP gene, prototype of a novel gene
 RT family encoding reticulons.";
 RL Genomics 32:191-199(1996).
 RN [3]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=98228245; PubMed=9560466;
 RA Hens J., Nuydens R., Geerts H., Senden N.H., Van de Ven W.J.M.,
 RA Roebroek A.J., van de Velde H.J., Ramaekers F.C., Broers J.L.;
 RT "Neuronal differentiation is accompanied by NSP-C expression.";
 RL Cell Tissue Res. 292:229-237(1998).
 CC -!- FUNCTION: MAY BE INVOLVED IN NEUROENDOCRINE SECRETION OR IN
 CC MEMBRANE TRAFFICKING IN NEUROENDOCRINE CELLS.
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=RTN1-A; Synonyms=NSP-A;
 CC IsoId=Q16799-1; Sequence=Displayed;
 CC Name=RTN1-B; Synonyms=NSP-B;
 CC IsoId=Q16799-2; Sequence=VSP_005644;
 CC Name=RTN1-C; Synonyms=NSP-C;
 CC IsoId=Q16799-3; Sequence=VSP_005645, VSP_005646;
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURAL AND NEUROENDOCRINE TISSUES
 CC AND CELL CULTURES DERIVED THEREFROM. EXPRESSION OF ISOFORM RTN1-C
 CC IS STRONGLY CORRELATED WITH NEURONAL DIFFERENTIATION.
 CC -!- PTM: ISOFORMS RTN1-A AND RTN1-B ARE PHOSPHORYLATED.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L10333; AAA59950.1; -.

DR EMBL; L10334; AAA59951.1; -.
 DR EMBL; L10335; AAA59952.1; -.
 DR PIR; A46583; A46583.
 DR PIR; I60904; I60904.
 DR Genew; HGNC:10467; RTN1.
 DR MIM; 600865; -.
 DR GO; GO:0030176; C:endoplasmic reticulum membrane, intrinsic p. . .; TAS.
 DR GO; GO:0004871; F:signal transducer activity; NAS.
 DR GO; GO:0030182; P:neuron differentiation; TAS.
 DR GO; GO:0007165; P:signal transduction; NAS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;
 KW Phosphorylation.
 FT TRANSMEM 603 623 POTENTIAL.
 FT TRANSMEM 726 746 POTENTIAL.
 FT DOMAIN 589 776 RETICULON.
 FT DOMAIN 609 612 POLY-LEU.
 FT VARSPLIC 1 420 Missing (in isoform RTN1-B).
 FT /FTid=VSP_005644.
 FT VARSPLIC 1 568 Missing (in isoform RTN1-C).
 FT /FTid=VSP_005645.
 FT VARSPLIC 569 588 GPGPLGPGAPPPLFLNKQK -> MQATADSTKMDCVWSNW
 FT KSQ (in isoform RTN1-C).
 FT /FTid=VSP_005646.
 SQ SEQUENCE 776 AA; 83617 MW; CA5B6232353096FE CRC64;

Query Match 13.5%; Score 789.5; DB 1; Length 776;
 Best Local Similarity 31.2%; Pred. No. 4.1e-23;
 Matches 243; Conservative 115; Mismatches 252; Indels 169; Gaps 28;

Qy 487 TSPKTSNPFVLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGT 546
 : | : | | : : : : | : | | : | : | :
 Db 65 SGPARGSP--VAMETASTGVAGVSSAMDHTFSTTSKDGEG-----SCYTSLI----S 110
 Qy 547 KIAYETKVDLVQTSEAIQ-ESLYPTAQLCPSPFEEAEATPSPVLPDI--VMEAPLNS---- 599
 | | : | : : | : : | | | | | : : | |
 Db 111 DICYPPEQEDSTYFTGILQKENGHVTISESP---EELGTPGPSLPDVPGLIESRGLFSSDSG 167
 Qy 600 --LLPSAGASVVQPSVSPLEAPPPVSY-----DSIKLEPENPPPYEEA-----M 641
 : | : | : | : | : : : | : : : | :
 Db 168 IEMTPAESTEVNKKILADPLDQMKAEAYKYIDITRPEEVKHKQEQHHPELEDKDLDFKNKDT 227
 Qy 642 NVALKALGTKEGIKEPE-----SFNAAVQETEAPYISACDLIKETKLSTE-PSP 690
 : : : | | : : | : : : | | | | | : | : : : : |
 Db 228 DISIK---PEGVREPDKPAPVEGKIIKDHLLLEESTFAPYID---DLSEEQRRAPIITP 280
 Qy 691 DFSNYSEIAKFEKSVPEHAELVEDSSPESEPVDLF-SDDSIPEV---PQTQEEAVMLMK 745
 : | | : | : : : | : | : | : | : : : :
 Db 281 VKITLLEIE-----PSVETTTQEKTPKQDICKLKPSPDTVPTVTVSEPEDDSPGSITPP 334
 Qy 746 ESLTEVSETVAQHK-----EERLSASQELGKPYLESFQP---NLHSTKDAASND---- 792
 | | | : | : : : : | : | : | : : : :
 Db 335 SSGTEPSAAESQGKGSISEDELITAIKEAKGLSYETAENPRPVGQLADRPEVKARSGPPT 394
 Qy 793 IPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKI----- 827

RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Eye, and Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN
 CC BRAIN. THREE TIMES MORE ABUNDANT IN MACULA THAN IN PERIPHERAL
 CC RETINA.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF059524; AAC99319.1; -.
 DR EMBL; AF059529; AAD20951.1; -.
 DR EMBL; AF059525; AAD20951.1; JOINED.
 DR EMBL; AF059526; AAD20951.1; JOINED.
 DR EMBL; AF059527; AAD20951.1; JOINED.
 DR EMBL; AF059528; AAD20951.1; JOINED.
 DR EMBL; AF119297; AAD26810.1; -.
 DR EMBL; BC000634; AAH00634.1; -.
 DR EMBL; BC010556; AAH10556.1; -.
 DR EMBL; BC011394; AAH11394.1; -.
 DR EMBL; BC022993; AAH22993.1; -.
 DR Genew; HGNC:10469; RTN3.
 DR MIM; 604249; -.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Transmembrane; Endoplasmic reticulum.
 FT TRANSMEM .68 88 POTENTIAL.

FT TRANSMEM 177 197 POTENTIAL.
 FT DOMAIN 48 236 RETICULON.
 SQ SEQUENCE 236 AA; 25609 MW; DDC6A4544ABCD7B7 CRC64;

Query Match 10.7%; Score 625.5; DB 1; Length 236;
 Best Local Similarity 59.1%; Pred. No. 1.4e-17;
 Matches 114; Conservative 41; Mismatches 37; Indels 1; Gaps 1;

Qy 972 SKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1031
 | : | | : : | | : | | | | | | : | : | | | | | | | | | | | | | | | |
 Db 44 SSCAVHDLIFWRDVKKTGTFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSV 103
 Qy 1032 IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLK 1091
 | | | : | | | : | | | | : | : : | | | | | : | : | : | : | | | | : | | | | |
 Db 104 IQAVQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHINRALKLIIRLFLVEDLVDLSLK 163
 Qy 1092 FAVLMWVFTYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKIDAMAKI 1151
 | | | | : | | | | : | | | | | : : | | : | : | : | : | | | | : | : | | : | |
 Db 164 LAVFMWLMTYVGAVFNGITLLILAEELLIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKI 223
 Qy 1152 QAKIPGL-KRKAD 1163
 | | | : | | : | : | :
 Db 224 QAKLPGIAKKKA 236

RESULT 7

RTN3_MOUSE

ID RTN3_MOUSE STANDARD; PRT; 237 AA.
 AC Q9ES97;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Reticulon protein 3.
 GN RTN3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang X., Zhou Y., Qiang H., Yuan J., Qiang B.;
 RT "Cloning and expression profile of a novel mouse cDNA encoding a human
 RT RTN3 homolog.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- SIMILARITY: Contains 1 reticulon domain.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AF195940; AAG31360.1; -.

DR MGD; MGI:1339970; Rtn3.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
KW Transmembrane; Endoplasmic reticulum.
FT TRANSMEM 69 89 POTENTIAL.
FT TRANSMEM 167 187 POTENTIAL.
FT DOMAIN 49 237 RETICULON.
SQ SEQUENCE 237 AA; 25428 MW; EB60A0A7AC45F0DE CRC64;

RESULT 8

CC Name=1; Synonyms=Brain;
CC IsoId=070622-1; Sequence=Displayed;
CC Name=2; Synonyms=Muscle;
CC IsoId=070622-2; Sequence=VSP_005650, VSP_005651;
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN NEURAL AND MUSCULAR
CC TISSUES.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF038537; AAC14906.1; -.
DR EMBL; AF038537; AAC14907.1; -.
DR EMBL; AF038538; AAC14908.1; -.
DR EMBL; AF038539; AAC14909.1; -.
DR EMBL; AF093624; AAD13195.1; -.
DR MGD; MGI:107612; Rtn2.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT TRANSMEM 295 315 POTENTIAL.
FT DOMAIN 272 471 RETICULON.
FT VARSPLIC 1 267 Missing (in isoform 2).
FT /FTid=VSP_005650.
FT VARSPLIC 268 271 PLLL -> MGSK (in isoform 2).
FT /FTid=VSP_005651.
SQ SEQUENCE 471 AA; 51346 MW; 9BBD8F372CF63AD3 CRC64;

Query Match 8.7%; Score 509; DB 1; Length 471;
Best Local Similarity 28.6%; Pred. No. 8.3e-13;
Matches 146; Conservative 84; Mismatches 175; Indels 106; Gaps 13;

QY 690 PDFSNYSEIAKFEKSVPEHAELVEDSSP--ESEPVDLFSDDSIPEVPQTQEEAVMLMKES 747
| |:: | |:: | | | | | |::|
Db 6 PVFAHCKEAPSTASSTPDSTEGNDDSDFRELHTAREFSED----- 46
QY 748 LTEVSETVAQH-----KEERLSASPQELGKPYLESFQPNLHST 785
| | |:: | : : : | : | | |
Db 47 --EEEETTSQDWGTPRELTFYSIAFDGVVSGGRRDSVVRPRPQGRSVSEPRDPPQSG 104
QY 786 KDAASNDIPTLTCK-----EKISLQMEEFNTAIYSNDDLSSKEDK 826
: | |:: | : : : | : | | |
Db 105 LGDSLESIPSLSQSPEPGRRGDPDPVPPAERPLEELRLRLDQLGWVVRS----AGSGED- 159
QY 827 IKESETFSDSSPIEIIDFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCL 886
| | |:: | : | : | : | | |:: | : |
Db 160 ----SATSSSTPLE--NEEPDGLLEASE-----AGEETNLEL----RLAQ-----SL 195
QY 887 ELPCDLSFKNIYPKDEVHVSDEFSENSSVSKASISPSNVSALEPQTEMGSIVKSKSLTK 946
| : : | : | | | : | : | : : : |
Db 196 HLQLEVLTPQLSPSSGTPQAHTPSPQRSQDSNS--GPDDEPLLNVVEEHWRLLEQEPITA 253


```

      | : | : | | : | | | | : |
Db      170 -----DEEP---QEPNRLETGEAGE-----EL--DLRLRLAQSSPE 201

Qy      904 HVSDEFSENRSSVSKASISP-----SNVSALEPQTE----- 934
      : : | : : | | | | |
Db      202 VLTPQLSPGSGTPQAGTPSPSRSDNSGPEEPLLEEEEEKQWGPLEREPVRGQCLDSTDQ 261

Qy      935 -----MGSIVK--SKSLTKEAEKKLP-----S 954
      : | : : | | | : |
Db      262 LEFTVEPRLLGTAMEWLKTSLLLA VYKTVPILELSPPLWTAIGWVQRGPTPTPVLRLVLL 321

Qy      955 DTEKEDRSLSAVLSAELSK---TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVT 1011
      | | | | | : | | | | : | : | | | : | | | |
Db      322 KWAKSPRS-SGVPSLSLGADMGSKVADLLYWKDTRTSGVVFTGLMVSLLLCLLHFSIVSVA 380

Qy      1012 AYIALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESEVAISEELVQKYSNSALGHVN 1071
      | : | | | | | | : | : | : | : | : | : | : | : | : | : |
Db      381 AHLALLLLCGTISLRVYRKVLQAVHRGDGANPFQAYLDVDLTLTREQTERLSHQITSRVV 440

Qy      1072 STIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQV 1131
      | : | | | | : | | | | | : | : | : | : | : | : | : | : |
Db      441 SAATQLRHFFLVEDLVDLSLKLALLFYILTFVGAIFNGLTLLILGVIGLFTIPLLYRQHQA 500

Qy      1132 QIDHYLGLANKSVKDAMAKIQAKIPG 1157
      | | | | : | | | : | | |
Db      501 QIDQYVGLVTNQLSHIKAKIRAKIPG 526

```

RESULT 10

PCLO_HUMAN

```

ID      PCLO_HUMAN      STANDARD;      PRT;      5147 AA.
AC      Q9Y6V0; O43373; O60305; Q9BVC8; Q9UIV2; Q9Y6U9;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Piccolo protein (Aczonin) (Fragments).
GN      PCLO OR ACZ OR KIAA0559.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE OF 1-759 FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=99439764; PubMed=10508862;
RA      Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,
RA      Kilimann M.W.;
RT      "Aczonin, a 550-kd putative scaffolding protein of presynaptic active
RT      zones, shares homology regions with rim and bassoon and binds
RT      profilin.";
RL      J. Cell Biol. 147:151-162(1999).
RN      [2]
RP      SEQUENCE OF 552-4404 FROM N.A.
RA      Kraemer J., Wollam C., Wohldmann P., McGrane B.;
RL      Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE OF 3619-5147 FROM N.A. (ISOFORM 2).

```

RC TISSUE=Brain;
 RX MEDLINE=98290545; PubMed=9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:31-39(1998).
 RN [4]
 RP SEQUENCE OF 4405-4439 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 4405-5147 FROM N.A.
 RA Kalicki J., Elliott G.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: May act as a scaffolding protein involved in the
 CC organization of synaptic active zones and in synaptic vesicle
 CC trafficking (By similarity).
 CC -!- SUBUNIT: Interacts with Rabac1/Pral and profilin (By similarity).
 CC -!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of
 CC synaptic junctions (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=Q9Y6V0-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9Y6V0-2; Sequence=VSP_003923, VSP_003924, VSP_003925,
 CC VSP_003926, VSP_003927;
 CC Note=No experimental confirmation available;
 CC -!- DOMAIN: C2 domain 1 is involved in binding calcium and
 CC phospholipids. Calcium binds with low affinity but with high
 CC specificity and induces a large conformational change.
 CC -!- SIMILARITY: Contains 2 C2 domains.
 CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; Y19188; CAB60727.1; -.
 DR EMBL; AC004903; AAD20936.1; -.
 DR EMBL; AC004886; AAD21789.1; -.
 DR EMBL; AB011131; BAA25485.1; -.
 DR EMBL; BC001304; AAH01304.1; -.
 DR EMBL; AC004082; AAB97937.1; -.
 DR PIR; T00634; T00634.
 DR HSSP; P04410; 1A25.
 DR Genew; HGNC:13406; PCLO.
 DR MIM; 604918; -.
 DR GO; GO:0005856; C:cytoskeleton; NAS.
 DR GO; GO:0045202; C:synaptic junction; ISS.
 DR GO; GO:0005509; F:calcium ion binding activity; ISS.
 DR GO; GO:0005544; F:calcium-dependent phospholipid binding acti. . . ; ISS.
 DR GO; GO:0005522; F:profilin binding activity; ISS.
 DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
 DR GO; GO:0016080; P:synaptic vesicle targeting; ISS.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001565; Synaptotagmin.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00399; SYNAPTOTAGMN.
 DR SMART; SM00239; C2; 2.
 DR PROSITE; PS00499; C2_DOMAIN_1; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 2.
 KW Calcium/phospholipid-binding; Zinc; Metal-binding; Zinc-finger;
 KW Repeat; Alternative splicing.
 FT NON_TER 1 1
 FT DOMAIN 400 465 10 X 10 AA TANDEM APPROXIMATE REPEATS OF
 FT P-A-K-P-Q-P-Q-Q-P-X.
 FT ZN_FING 499 523 C4-TYPE (POTENTIAL).
 FT ZN_FING 969 992 C4-TYPE (POTENTIAL).
 FT NON_CONS 1010 1011
 FT DOMAIN 2300 2325 POLY-PRO.
 FT DOMAIN 4391 4442 PDZ.
 FT DOMAIN 4544 4633 C2 DOMAIN 1.
 FT DOMAIN 5031 5121 C2 DOMAIN 2.
 FT VARSPLIC 4404 4404 S -> SGNGLGIRIVGGKEIPGHSGEIGAYIAKILPGGSAE
 FT QTGKLMEG (in isoform 2).
 FT /FTId=VSP_003923.
 FT VARSPLIC 4534 4534 K -> KPTDGTKVVSHPITGEIQ (in isoform 2).
 FT /FTId=VSP_003924.
 FT VARSPLIC 4576 4576 G -> GQVMVVQNAS (in isoform 2).
 FT /FTId=VSP_003925.
 FT VARSPLIC 4757 4761 TAHKS -> SKRRK (in isoform 2).
 FT /FTId=VSP_003926.
 FT VARSPLIC 4762 5147 Missing (in isoform 2).
 FT /FTId=VSP_003927.
 SQ SEQUENCE 5147 AA; 563537 MW; CD5D84990498CD3C CRC64;

Query Match 5.3%; Score 308.5; DB 1; Length 5147;
 Best Local Similarity 21.4%; Pred. No. 0.00065;
 Matches 264; Conservative 150; Mismatches 438; Indels 383; Gaps 63;

```

Qy      3 DIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEDEEDEDLEEEVLERKPA 62
      || : | | || : || : : | : : : | : ||
Db    251 DIVRGESVKPSLPSPSKPP-----IQQTPGKPPAQQPGHEKSQPG-----PAKPP 296

Qy     63 AGLSAAAVP----PAAAAPLLDFSSDSVPPA-PRGPLPAAPPA-----A 101
      | | | | | : | : || | | | || || |
Db    297 AQPSGLTKPLAQPGTVKPPVQPPGTTKPPAQPLG--PAKPPAQQTGSEKPSSEQPGPKA 354

Qy    102 PERQPSWERSPA-APAPSLP-----PAAAVLPSKLPEDDEPPA--- 138
      : | : : || | | : | | | | | : | : | : || :
Db    355 LAQPPGVGKTPAQQPGPAKPPTQQVGT PKPLAQQPGLOSPAKAPGPTKTPTAQTKPPSQQP 414

Qy    139 ---RPPPPPPAGASPLAEPAAPPSTPAAPKRRSGSVDETLFALPAASEPVI PSSAEKIM 195
      : || | | | | | | || : : || | | : | : | : || :
Db    415 GSTKPPPQQPGPAKP--SPQQPGSTKPPSQQPGS-----AKPSAQQ---PSPAKPSA 461

Qy    196 DLMEQPGNTVSSGQEDFPSVLLETAASLPS-----LSPL-STVSFKEH-GYLGNL SAVS 247
      : | : | : | : : | || : || : | | | : :
Db    462 QQFTKPVSTGFGKPLQPPTVSPSAKQPPSQGLPKTICPLCNTTELLLLHVPEKANFNTCT 521

Qy    248 SSEGTI-----EETLNEASKEL-----PERATNPVFNVDL 277
      : | : | || : | | : | |
Db    522 ECQTTVCSLCGFNPNPHLTEAKEWLCNLCQMKRALGGDLAPVPSSPQPKLKTAPVTTTSA 581

Qy    278 AEFSELEYSEMGSFSGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGK 337
      | : : : || : : | | : : : | : | : |
Db    582 VSKSSPQQQTSPKKDAAPKQDLSKAPEPKPPPLVKQPTLHGSPSAKAKQPPEADSLSK 641

Qy    338 EDRVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAWVEVKDTEGSRDVLAAARANVES 397
      : | | : : | || | || || : | || | : | : | :
Db    642 P----APPKEPSVPSEQDK---APV----ADDKP-KQPKMVKPTTD---LVSSSSATTKP 686

Qy    398 KVDRKCLEDLSLEQKS---LGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTT 454
      : : : | : | || : : || | | | | |
Db    687 DIPSSKVQSQAEKTTPLPKTDSAKPSQ--SFPPTGEKV-----TPFD SKAI PRP 734

Qy    455 ANTFFP LLE--DHTSENKTD-----EKKIEERKAQIIITEKTSPK----- 490
      | : : : || : | : || | : || | | || |
Db    735 ASDSKIISHPGPSSSESKGQKQVDPVQKKEEPKKAQ---TKMSPKPDAPMPKGSPTPPGP 791

Qy    491 --TSNPFLVAVQDS----EADYVTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEAT 544
      | : : | | | : | : | : | | | | |
Db    792 RPTAGQTVPTPQQSPKPQEQRFRSLNLGSITDAPKSQ-----PTTPQET-----VT 838

Qy    545 GTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSA 604
      | : : | | | : | | : | : | : | : | :
Db    839 GKLF GFGASI-FSQASNLISTAGQPG----PHSQSGPGAP-----MKQAPAPSQPPTS 886

Qy    605 GASVVQPSVSPLEAPP-----PVS YD-----SIKLEP-----ENPPPYEE 639
      | | : || | | : : : || | | : || | :
Db    887 QG----PPKSTGQAPPAPAKSIPVKKETKAPAAEKLEPKAEQAPT VKRTETEKKPPPIKD 942

Qy    640 AMNVALK----ALGTK-----EGIKEPESFNAAVQ-----E 666

```

```

      : :: :      | | |      | | : | : | |      :
Db      943 SKSLTAEPQKAVLPTKLEKSPKPESTCPLCKTELNIGSKDPNPNFTCTECKNQVCNLCGF 1002

Qy      667 TEAPYISIIAC-----DLIK-----ETKLSTEPSPDFSNYSEIAKFEKSVPEHA 709
      | :: : |      | : |      | | | |      : | : : : | |
Db      1003 NPTPHLTENCQTQRAISGQLGDIRKMPPAPSGPKASPMFVP-----TESSSQKTAVPPQV 1057

Qy      710 ELV----EDSSPESEPV-----DLFSDDSIPEV---PQTQEEAVMLMKESLTEVSETVA 756
      : | |      : : | : |      : | : | | : | | | : | | : : : |
Db      1058 KLVKKQEQEVKTEAEKVILEKVKETLSMEKIPPMVTTDQKQES-KLEKDKASALQEKKP 1116

Qy      757 QHKEERLSASPQEL---GKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTA 812
      : | :: |      : :: | | | : |      | : | | | : |
Db      1117 LPEEKKLIPEEKIRSEEKKPLLEKKPTPEDKK-----LLPEAKTSAPEEQ---- 1163

Qy      813 IYSNDDLSSK----EDKI-----KESETFSDSSPIEIIDFPTFVSAKDDS- 855
      | | | | : : | : | :      | : : | : |      | : : : | |
Db      1164 ---KHDLLKSQVQIAEEKLEGRVAPKTVQEGKQPQTKMEGLP----SGTPQSLPKEDDKT 1216

Qy      856 -----PKLAKEYTDLEVS DKSEIANIQ-----SGADSLPCLELPCD 891
      | | | : | | | : : |      | | | : | : |
Db      1217 TKTIKEQPQPPCTAKPDQEKE-DDKSDTSSSQQPKSPQGLSDTGYSDDGISSSLGEIP-- 1273

Qy      892 LSFKNIYPKDEVHV-----SDEFSENRSSVSK---ASISPSNVSALEPQTEMGSIVKSKS 943
      : : | | | : | | | : | | : : : | | | : | | :
Db      1274 ----SLIPTDEKDILKGLKKDSFSQESSPSSPSDLAKLESTVLSILEAQASTLADEKSEK 1329

Qy      944 LTK--EAEKKLPSDTEKEDRSLSAVLSAELSKTSV 976
      | : | : | | | : | | | : | : :
Db      1330 KTQPHEVSPEQPKDQEK-TQSLSETLEITISEEEI 1363

```

RESULT 11

PCLO_CHICK

```

ID   PCLO_CHICK      STANDARD;          PRT;   5120 AA.
AC   Q9PU36;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Piccolo protein (Aczonin) (Fragment).
GN   PCLO OR ACZ.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=99439764; PubMed=10508862;
RA   Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,
RA   Kilimann M.W.;
RT   "Aczonin, a 550-kd putative scaffolding protein of presynaptic active
RT   zones, shares homology regions with rim and bassoon and binds
RT   profilin.";
RL   J. Cell Biol. 147:151-162(1999).
CC   !- FUNCTION: May act as a scaffolding protein involved in the

```

```

CC      organization of synaptic active zones and in synaptic vesicle
CC      trafficking (By similarity).
CC      -!- SUBUNIT: Interacts with Rabac1/Pral and profilin (By similarity).
CC      -!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of
CC      synaptic junctions (By similarity).
CC      -!- DOMAIN: C2 domain 1 is involved in binding calcium and
CC      phospholipids. Calcium binds with low affinity but with high
CC      specificity and induces a large conformational change.
CC      -!- SIMILARITY: Contains 2 C2 domains.
CC      -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; Y19187; CAB60725.1; -.
DR      HSSP; P04410; 1A25.
DR      GO; GO:0045202; C:synaptic junction; ISS.
DR      GO; GO:0005509; F:calcium ion binding activity; ISS.
DR      GO; GO:0005544; F:calcium-dependent phospholipid binding acti. . .; ISS.
DR      GO; GO:0005522; F:profilin binding activity; ISS.
DR      GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
DR      GO; GO:0016080; P:synaptic vesicle targeting; ISS.
DR      InterPro; IPR000008; C2.
DR      InterPro; IPR001478; PDZ.
DR      InterPro; IPR001565; Synaptotagmin.
DR      Pfam; PF00168; C2; 2.
DR      Pfam; PF00595; PDZ; 1.
DR      PRINTS; PR00399; SYNAPTOTAGMN.
DR      SMART; SM00239; C2; 2.
DR      SMART; SM00228; PDZ; 1.
DR      PROSITE; PS00499; C2_DOMAIN_1; 1.
DR      PROSITE; PS50004; C2_DOMAIN_2; 2.
DR      PROSITE; PS50106; PDZ; 1.
KW      Calcium/phospholipid-binding; Zinc; Metal-binding; Zinc-finger;
KW      Repeat.
FT      NON_TER      1      1
FT      DOMAIN      258      357      10 X 10 AA TANDEM APPROXIMATE REPEATS OF
FT                                     P-A-K-P-Q-P-Q-Q-P-X.
FT      ZN_FING      368      392      C4-TYPE (POTENTIAL).
FT      ZN_FING      836      859      C4-TYPE (POTENTIAL).
FT      DOMAIN      2324      2343      POLY-PRO.
FT      DOMAIN      4414      4493      PDZ.
FT      DOMAIN      4627      4726      C2 DOMAIN 1.
FT      DOMAIN      5003      5094      C2 DOMAIN 2.
SQ      SEQUENCE      5120 AA; 560751 MW; A658D9891B65B412 CRC64;

```

```

Query Match          5.1%; Score 300; DB 1; Length 5120;
Best Local Similarity 20.4%; Pred. No. 0.0014;
Matches 258; Conservative 152; Mismatches 464; Indels 388; Gaps 56;

```

```

Qy      14 TDSPPRPPPAFKYQFVTEPEDEEDEEE-----EEDEEEDDEDLEELEVLERKPAAGLSAA 68
      :||      | : | ||: | : ||:      ::: : ::: : : | :

```

Db 90 SDSDAAHEEAGRKQKVTQKEQGKPEEQRGLAKHPSQQQSPKLVQQQGPVKPTPQQTESSK 149
 Qy 69 AVP-----PAAAAPLLDFSSDSV--PPAPRGP---LPAAPPAAPERQPSWE 109
 || : | | : | | | | | : | | : |
 Db 150 PVPQQQQPGEPKQGQKPGPSHP-GDSKAEQVKQPPQPRGPKSQLQQSEPTKPGQQQTSA 208
 Qy 110 RSPAAPAPSLP--PAAAVLPSKLPEDDEP-----PAR-----P 140
 : | | | | : | | : | | | |
 Db 209 KTSAGPTKPLPQQPDSAKTSSQAPPPTKPSLQQSGSVKQPSQQPARQGGPVKPSAQQAGP 268
 Qy 141 PPPPPAGASPLAEPAAAPPSTPAAPKRRSGSGVDET--LFALPAASEPVI PSS--AEKIMD 196
 | : | | | : | | | : : | : : | | | |
 Db 269 PKQQPGSEKPTAQQTGPAKQPPQP-GPGKTPLQQTGPVKQVPPQAGPTKPSQTAGAAKS 327
 Qy 197 LMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLGNLSAVSSSEGTIEET 256
 | : | | | | : | | : : | : : | | : |
 Db 328 LAQQPGGLTKPPGQQPGPEKPLQQKQA-----STTQPVESTPKKT 366
 Qy 257 L-----NEASKELPERAT-----NPFVNRDLAEFSE-----LEYS 286
 | | | : | | | : : |
 Db 367 FCPLCTTTTELLLTPEKANYNTCTQCHTVVCSLCGFNP--NPHITEIKEWLCLNCQMORA 424
 Qy 287 EMGSSFKGSPKGESAILVENTKEEVI VRSKDKEDLVCSAALHSPQESPVGKEDRVVSPE- 345
 | | | : | | | | | | | : | : |
 Db 425 LGGDLASGHGPGPQ-----LPPPKQKTPTPASTAKPSPQLQPGQKKDASPKPDP 473
 Qy 346 -----KTMDIFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAARANVESK 398
 | : : | | : : : | : : | | : |
 Db 474 SQQADSKKPVPQKKQPSMPGSPPVKSKQTHAEPSTGQQI-DSTPKSDQVKPTQA----- 527
 Qy 399 VDRKCLEDSEQKSLGKD-----SEGRNEDASFPSTPEPVKDSRRAYITCASFTSA 449
 | : | | : | : | : | : | : | : | : |
 Db 528 -----EEKQNQPSIQKPTMDTVPTSAAPGVKQDLADPQSP-----STQQKVTDSPMPET 576
 Qy 450 TESTTANTFPLLEDHTSENKTDEKKIEERKAQII TEKTSP-----KTSNPFV 497
 | : | : | : | : | : | : | : | : | : |
 Db 577 TK-----PPADTHPAGDKPDSKPL----PQVSRQKSDPKLASQSGAKSDAKTQKPSEP 625
 Qy 498 A-VQDSEADYVT-----TDTLSKVTEAAVSNMPE----- 525
 | | : | | : | : | : | : | : |
 Db 626 APVKDDPKKIQTKPAPKPDTPAPKGPQAGTGPRPTSAQPAPQPQQPQKTPEQSRFSLN 685
 Qy 526 --GLT-----PDLVQEACESEL-----NEA-----TGTKIAYETKVDLVQTSEAIQ 564
 | : | | | : | : | : | : | : | : | : |
 Db 686 LGGITDAPKPQPTTPQETVTGKLFGFGASIFSQASSLISTAGQPGSQTSGPAPPATKQPQ 745
 Qy 565 ESLYPTAQLCPSFEEAEATPSP-VLPDIVMEAPLNS--LLPSAGASVVQPSVSPLEAPPP 621
 | | | | : | | | | | | | : | | | |
 Db 746 PPSQPPASQAPPKEAAQAQPPPKAAPTKKETKPLASEKLGPMASDSTLTTKGSDLEKKPS 805
 Qy 622 VSYDSIKLEPENPPPYE-----EAMNVALKALGTKEGIEPESFNAA----- 663
 : : | | | | : : | | | | : | : | : |
 Db 806 LAKDSKHQTAEAKKPAELSEQEASQPKVSCPLCKTGLNIGSKDPPNFNTCTECKKVVCN 865
 Qy 664 -----VQETEAPYISIA-----DLIK----- 680
 | | : : | : | : | : | : | : |
 Db 866 LCGFNPMPHIVEVQE---WLCLNCQTQRAMSGQLGDMGKVPLPKLGPSQPVSKPPATPQ 921

Qy 681 -----ETKLSTEPSPDFSNYSEIAKFEKSVP--EHAEL-----VEDSS 716
 Db 922 KQPVPAVSHSPQKSSTPPTPAATKPKEEPSVPKEVPKLQQGKLEKTLSDAKIQQGIQKED 981
 Qy 717 PESEPVDLF---SDDSIPEVPQTQEEAVMLMKESLTVSETVAQH-KEERLSASPQELGK 772
 Db 982 AKSKQGKLFKTPSADKIQRVSQKEDSRLQQTKLTKTPSSDKILHGVQKEDIKFQEAKLAK 1041
 Qy 773 -----PYLESFQPNLHSTKDA---ASNDIPTLTKEKISLQMEEFNTAIYSN----- 816
 Db 1042 IPSADKILHRLQKEDPKLQQMKMAKALSADKIQPEAQKEDVQLQEVRLSKAVSADKIQHG 1101
 Qy 817 --DDL-----LSSKEDKI---KESETFSDSSPIEII-DEFPTFVSA----- 851
 Db 1102 IQKDLNLQHVKIEKTSSVEKIQEAQKESKLQQDKLPKTLSEDKIPATVSSDHKKLLSKSE 1161
 Qy 852 KDDSPKLAKEYTDLEVSDKSEIANIQSG--ADSLPCLELPCDLSFKNIYPKDEVHVSDE- 908
 Db 1162 EDKKPELLEKSTPHPKDKKEQITAETTGHI TEQKVEVEAPCD----KLHEKKQEDVKKED 1217
 Qy 909 ----FSENRSSVSKA--SISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRS 962
 Db 1218 LTTGIPQMVSKEPEAEBEKTPVPVSRL-PRSDHVEAVREK-IEKEDDK--SDTSSSQQQ 1272
 Qy 963 LS 964
 Db 1273 KS 1274

RESULT 12

CPN_DROME

ID CPN_DROME STANDARD; PRT; 865 AA.
 AC Q02910;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Calphotin.
 GN CPN OR CAP.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=93165729; PubMed=8094559;
 RA Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
 RT "Calphotin: a Drosophila photoreceptor cell calcium-binding protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=93165730; PubMed=8434015;
 RA Ballinger D.G., Xue N., Harshman K.D.;
 RT "A Drosophila photoreceptor cell-specific protein, calphotin, binds

RT calcium and contains a leucine zipper.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).
 CC -!- FUNCTION: Might function as a calcium-sequestering "sponge" to
 CC regulate the amount of free cytoplasmic calcium. It binds 0.3 mole
 CC of Ca(2+) per mole of protein.
 CC -!- SUBUNIT: Homodimer (Probable).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC; HYPODENSE COMPARTMENT.
 CC -!- TISSUE SPECIFICITY: SOMA AND AXONS OF PHOTORECEPTOR CELLS OF
 CC COMPOUND EYES AND OCELLI.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED EARLY IN PHOTORECEPTOR CELL
 CC DEVELOPMENT.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; L02111; AAA28405.1; -.
 DR EMBL; L05080; AAA28420.1; -.
 DR PIR; A47282; A47282.
 DR PIR; A47283; A47283.
 DR FlyBase; FBgn0010218; Cpn.
 DR GO; GO:0005509; F:calcium ion binding activity; IDA.
 KW Calcium-binding.

FT	CONFLICT	36	36	A -> AVAPAVVA (IN REF. 2).
FT	CONFLICT	43	43	I -> T (IN REF. 2).
FT	CONFLICT	64	64	I -> V (IN REF. 2).
FT	CONFLICT	76	76	T -> A (IN REF. 2).
FT	CONFLICT	100	100	P -> PP (IN REF. 2).
FT	CONFLICT	126	127	VQ -> AP (IN REF. 2).
FT	CONFLICT	154	154	I -> V (IN REF. 2).
FT	CONFLICT	160	160	S -> T (IN REF. 2).
FT	CONFLICT	534	534	A -> E (IN REF. 2).
FT	CONFLICT	699	699	I -> T (IN REF. 2).
FT	CONFLICT	703	703	V -> L (IN REF. 2).
FT	CONFLICT	721	721	D -> E (IN REF. 2).
SQ	SEQUENCE	865 AA;	84781 MW;	2110417E0B0E7CFE CRC64;

Query Match 5.1%; Score 295.5; DB 1; Length 865;
 Best Local Similarity 21.3%; Pred. No. 0.00021;
 Matches 217; Conservative 127; Mismatches 379; Indels 295; Gaps 41;

Qy	62	AAGLSAAAVPPAAAPLLDFSSDSVPPAPRGPLPAAPPAAPER----	QPSWERSPAAPAP	117
		: :: : :		
Db	11	SAPVAAPVTPSAVAAPVQVVSPAAVAPAPAAPIAVTPVAPPPTLASVQPATVTIP-APAP		69
Qy	118	----SLPPAAAVLPSKLPEDDEPPARPPPPPPAGA-----	SPLAEPAAPSTP----	161
		: :		
Db	70	IAAASVTPVASVAPPVVAAPTTPAASPVSTPVAVAQIPVAVSAPVAPPVAATPTPVVQIP		129
Qy	162	-AAPKRRGSGSVDETLFALP--AASEP----	VIPSSAEKIMDLMEQPGNT---VSSGQED	211
		: :		
Db	130	VAAP-----VIATPPVAASAPTAAVTPVISPVIASPPVVPANTTTPVAAPVAA		178

Qy	212	FPSVLLLETAASL-PSLSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLINEASKELPERATN	270
Db	179	VPAAVPVVAPVLAPAVAPAVAPVVAETPAPPPVAEIPVA--TIPECVAPLIPEVSVVATK	236
Qy	271	PFVNRDLAEFSELEYSEMGSFSGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSP	330
Db	237	PLA-----AAEPVVVAPPATETPVVAPAAASP	263
Qy	331	QESPVGKEDRVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAWEVKDTYEGSRDVLA	390
Db	264	HVS-----VAP-----AVETAVVAPV-----	279
Qy	391	ARANVESKVDRKCLEDSEQKSL----GKDSEGRNEDASFPSTPEPVKDSSRAYITCASF	446
Db	280	-SASTEPVAAATLTTPAPETPALAPVVAESQVAANTVVATPPTPAPEPETIAPPVVAETP	338
Qy	447	TSATESTTANTFPLLEDHTSENKTDEKKIEERKAQIIITEKTSPKTSNPFLVAVQDSEADY	506
Db	339	EVASVAVAETTPPVVPPVAAES-----IPAPVVATTVPATLAVTDPD---	381
Qy	507	VTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQES	566
Db	382	-----VTASAVPELPPVIAPSPVPSA-----VAETPVDLA-----PPV	414
Qy	567	LYP-TAQLCPSF--EEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAP----	619
Db	415	LPPVAAEPVPAVVAEETPETPAPASAPVTI-AALD--IPEVAPVIAAPSDAPAEAPSAAA	471
Qy	620	PPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESFNAAVQTEAPYISIACD--	677
Db	472	PIVS-----TPPT-----TASVPETTAPPAAVPTEPI	498
Qy	678	---LIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAE--LVEDSSPESEFVDLFSD-DSIP	731
Db	499	DVSVLSEAAIETPVAPPVEVTTEVAVADVAPPEAAADLIEPVEPPAPIPDLLEQTTTSPV	558
Qy	732	EVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQPNLHSTKDAASN	791
Db	559	AVEAAESTSSPIPETSLPPPNEAVA--SPEVAVAPITAPEPIPEP-EPSLATPTEPIPV	614
Qy	792	DIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSOSSPIEIDEFPTFVSA	851
Db	615	EAPV-----VIQEAVDAVEVPVTETSTSIPETTVEFPEAVAE	651
Qy	852	KDDSPKLAKEYTDLEV-SDKSEIANIQSGAD----SLPCLEL-----PCDLSFKNIYP-	899
Db	652	KVLDPAI----TEAPVTTQEPDVANINDGAPATEITTPAVEIVTAAAEVSDIAIPVIDPP	707
Qy	900	-KDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMG-----	936
Db	708	VPQEIAVA-EIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAAEVPITAGDN	766
Qy	937	----SIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGV	990
Db	767	PDNTSVGISEVVPTIAEKPVEEVPTSEIPEQSSSPSDSVPAKITPLL--RDLQTTDV	822

RESULT 13

MAPB_RAT

ID MAPB_RAT STANDARD; PRT; 2459 AA.
AC P15205; Q62958; Q9ER21; Q9QW92;
DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Microtubule-associated protein 1B (MAP 1B) (Neuraxin) [Contains: MAP1
DE light chain LC1].
GN MAP1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-142 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=96257242; PubMed=8666295;
RA Liu D., Fischer I.;
RT "Isolation and sequencing of the 5' end of the rat microtubule-
RT associated protein (MAP1B)-encoding cDNA.";
RL Gene 172:307-308(1996).
RN [2]
RP SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION.
RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Glial tumor;
RX MEDLINE=92347374; PubMed=1639092;
RA Zauner W., Kratz J., Staunton J., Feick P., Wiche G.;
RT "Identification of two distinct microtubule binding domains on
RT recombinant rat MAP 1B.";
RL Eur. J. Cell Biol. 57:66-74(1992).
RN [3]
RP SEQUENCE OF 1541-2459 FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Spinal cord;
RX MEDLINE=90059871; PubMed=2555150;
RA Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,
RA Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H.;
RT "Neuraxin, a novel putative structural protein of the rat central
RT nervous system that is immunologically related to microtubule-
RT associated protein 5.";
RL EMBO J. 8:2879-2888(1989).
RN [4]
RP DEVELOPMENTAL STAGE, AND PHOSPHORYLATION.
RX MEDLINE=97405699; PubMed=9260743;
RA Ma D., Nothias F., Boyne L.J., Fischer I.;
RT "Differential regulation of microtubule-associated protein 1B (MAP1B)
RT in rat CNS and PNS during development.";
RL J. Neurosci. Res. 49:319-332(1997).
CC -!- FUNCTION: The function of brain MAPS is essentially unknown.
CC Phosphorylated MAP1B may play a role in the cytoskeletal changes
CC that accompany neurite extension. Possibly MAP1B Binds to at least
CC two tubulin subunits in the polymer, and this bridging of subunits
CC might be involved in nucleating microtubule polymerization and in
CC stabilizing microtubules.
CC -!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
CC with MAP1A and MAP1B proteins.
CC -!- TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem,
CC cerebellum and cerebrum). Not expressed in liver, spleen, kidney,

CC heart or muscle.
 CC -!- DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic
 CC nerve levels are high early in development but decrease during
 CC postnatal development and are low in adults. In dorsal root
 CC ganglia levels remain high throughout development.
 CC -!- INDUCTION: By nerve growth factor.
 CC -!- DOMAIN: Has a highly basic region with many copies of the sequence
 CC KKEE and KKEI/V, repeated but not at fixed intervals, which is
 CC responsible for the binding of MAP1B to microtubules.
 CC -!- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated
 CC from MAP1B by proteolytic processing. It is free to associate with
 CC both MAP1A and MAP1B. It interacts with the amino-terminal region
 CC of MAP1B (By similarity).
 CC -!- PTM: Phosphorylated.
 CC -!- SIMILARITY: TO MAP1A.
 CC -!- CAUTION: A C-terminal fragment of this protein (residues 1597 to
 CC 2459) was originally described as neuraxin in Ref.3.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U52950; AAB17068.1; -.
 DR EMBL; X60370; CAC16162.1; -.
 DR EMBL; X16623; CAA34620.1; ALT_SEQ.
 DR PIR; A56577; A56577.
 DR InterPro; IPR000102; MAP1B_neuraxin.
 DR Pfam; PF00414; MAP1B_neuraxin; 10.
 DR PROSITE; PS00230; MAP1B_NEURAXIN; 8.
 KW Microtubules; Repeat; Phosphorylation.
 FT CHAIN ? 2459 MAP1 LIGHT CHAIN LC1.
 FT REPEAT 1869 1885 MAP1B 1.
 FT REPEAT 1886 1902 MAP1B 2.
 FT REPEAT 1903 1919 MAP1B 3.
 FT REPEAT 1920 1936 MAP1B 4.
 FT REPEAT 1937 1953 MAP1B 5.
 FT REPEAT 1954 1970 MAP1B 6.
 FT REPEAT 1988 2004 MAP1B 7.
 FT REPEAT 2005 2021 MAP1B 8.
 FT REPEAT 2022 2038 MAP1B 9.
 FT REPEAT 2039 2055 MAP1B 10.
 FT DOMAIN 559 1035 GLU-RICH.
 FT DOMAIN 588 786 LYS-RICH (HIGHLY BASIC, CONTAINS MANY
 FT KKEE AND KKEI/V REPEATS).
 FT LYS-RICH.
 FT DOMAIN 2224 2312
 FT CONFLICT 127 127 M -> V (IN REF. 1).
 FT CONFLICT 140 140 T -> S (IN REF. 1).
 FT CONFLICT 2112 2112 R -> K (IN REF. 3).
 FT CONFLICT 2169 2169 L -> I (IN REF. 3).
 SQ SEQUENCE 2459 AA; 269497 MW; 2E3F6872DEDB8BA2 CRC64;

Query Match 5.0%; Score 291.5; DB 1; Length 2459;
 Best Local Similarity 20.0%; Pred. No. 0.0011;

Matches 220; Conservative 167; Mismatches 456; Indels 255; Gaps 44;

```
Qy      30 TEPEDDEEEEEDEEDEDLEEEVLERKPAAGLSAAAVPPAAAAPLLDSSSDSVPPA 89
      :| | | | : : | | | : : : | | | | | : : | :
Db     1008 SEEEGEEEEEDKAEDAREEDHEPDKTE-----AEDYVMAVVDKAAEAGVTEDQYDFL--- 1058

Qy      90 PRGPLPAAPPAAPERQPSWERSPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPPPAGAS 149
      | : | | : | | | : : | | | | | |
Db     1059 -----GTPAKQ-----PGVQSPSREPASSIHDETLPGGSESEAT-----AS 1094

Qy     150 PLAEPAPPSTPAAPKRRGSGSVDETLFALPAASEPVIPSSAEKIMDLMEQPGN---TVS 206
      | | | | | | | : : | | | | | |
Db     1095 DEENREDQPEEFTAT---SGYTQST---IEISSEPTPMDEMSTPRDVMTDETNNETES 1147

Qy     207 SGQE-----DFPSVLLETAASLP---SLSPLS---TVSFKEHGYLGNLSAVSSSEG TIE 254
      | | | | | | | | | | | | | : : | : | : |
Db     1148 PSQEFVNITKYESSLYSQEYSKPVVASFNGLSDGSKTDATDGRDYNASASTISPPSSMEE 1207

Qy     255 ETLNEAS-----KELPERATNPFVNRDLAEF--SELEYSEMG--- 289
      : : : : | : : : | : : | : | : : |
Db     1208 DKFSKSALRDAYRPEETDVKTGAELDIKDVSDERLSPAKSPSLSPSPSPPIEKTPLGERS 1267

Qy     290 -----SSFKGSPKGESAILVENTKEEVIVR---SKDKEDL-----VCSAALHSP 330
      : | | : | | : | : : | : : | : | : |
Db     1268 VNFSLTPNEIKASAEGEATAVSPGVTQAVVEEHCASPEEKTLEVVSQSVTGSAGHTP 1327

Qy     331 -QESPVGKEDRVVSPEKTMDFNEMQMSVVAPVREEYADFK-----PFEQAWEVKD 380
      : | | : : : | | : : | | : : | : : |
Db     1328 YYQSPTDEKSSHLPTTEVT-----ENAQAVPVSFTEAKDENERSSISPMDE--PVPD 1378

Qy     381 TYEGSRDVLAAARANVESKVDRKCLED--SLEQKSLGKDS---EGRNEDASFPSTPEPVK 434
      : | | : : | | | : : | | : | | | |
Db     1379 SESPIEKVLSPLRSPPLIGSESAYEDFLSADDKALGRRSESPFEGKNGKQGFSDKESPVS 1438

Qy     435 DSSRAYITCASFTSATESTTANTFPLLEDHTSENKT-----DEKKI----- 475
      | : | : | | | | : | | | | | | |
Db     1439 D-----LTSDLYQDKQEEKRAGFIPIKEDFSPEKKASDAEIMSSQSALALDERKLGGDGS 1493

Qy     476 -----EERKAQIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAV-- 520
      | : | | | | : | : | : | : : | : |
Db     1494 PTQVDVSQFGSFKEDTKMSISEGTVSDKSATPVDEGAEDT--YSHMEGVASVSTASVAT 1550

Qy     521 SNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQES-LYPTAQLCP---S 576
      | : | | | | : : | : | : | | | | : : | : |
Db     1551 SSFPEPTTDD-VSPSLHAEVGSPPHSTEVDDSLSVSVVQTPTTFQETEMSPSKEECPRPMS 1609

Qy     577 FEEAEATP-----SPVLPDIVMEAPLNSLL-----PSAGASVVQ 610
      : : | : : : | : | : | | : | | :
Db     1610 ISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSLAMDFSRQSPDHPTVGAGMLH 1669

Qy     611 PSVSPLEAPPPVSYD-----SIKLEPENPPPYEEAMNVALKALGTKEGIKEPESFN 661
      : : | | | | | : | | | | : : : : : :
Db     1670 ITEN---GPTEVDYSPSDIQDSSLSHKIPPTTEPSYTDNDLS-ELISVSQVEASPSTSS 1725

Qy     662 AAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESEP 721
      | | | : | | | | : : | : | | : |
Db     1726 AHTPS-----QIASPLQEDTLSDVVPVPRDMSLYASLASEKVQSLEGEKL----SPKSDI 1775
```

Qy 722 VDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYL-ESFQP 780
 Db 1776 SPLTPRESSPTYSPGFSDSTSGAKES-TAAYQTSSSPPIDAAAAEPYGFRSSMLFDTMQH 1834

Qy 781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDIKESETFSDSSPIE 840
 Db 1835 HLALSRDLTTSSV----EKDNGGKTPGDFNYAYQKPESTTESPDEEDYDYE--SHEKTIQ 1888

Qy 841 IIDEFPTFVSAKDDSPK----LAKEYTDLEVSDKSEIANIQSGADSLPCLLELPDLSFKN 896
 Db 1889 AHDVGGYYYEKTERTIKSPCDSGYSYETIEKTTKTP-----EDGGYS-----CEITEKT 1937

Qy 897 IYPKDEVHVSDEFSENRSSVSKAS-----ISPSNVSALEPQTEMGSIVKSKSL 944
 Db 1938 TRTPEEGGYSEISEKTTTRTPEVSGYTYEKTERRRLLDDISNGYDDTEDGGHTLGDCSY 1997

Qy 945 TKEAEKKLPDTEKEDRS 962
 Db 1998 SYETTEKITSFPESESYS 2015

RESULT 14

MAPB_HUMAN

ID MAPB_HUMAN STANDARD; PRT; 2468 AA.
 AC P46821;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Microtubule-associated protein 1B (MAP 1B) [Contains: MAP1 light chain LC1].
 GN MAP1B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=95104835; PubMed=7806212;
 RA Lien L.L., Feener C., Fischbach N., Kunkel L.M.;
 RT "Cloning of human microtubule-associated protein 1B and the
 RT identification of a related gene on chromosome 15.";
 RL Genomics 22:273-280(1994).
 CC !- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.
 CC PHOSPHORYLATED MAP1B MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES
 CC THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAP1B BINDS TO AT LEAST
 CC TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS
 CC MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
 CC STABILIZING MICROTUBULES.
 CC !- SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE
 CC WITH MAP1A AND MAP1B PROTEINS.
 CC !- DOMAIN: Has a highly basic region with many copies of the sequence
 CC KKEE and KKEI/V, repeated but not at fixed intervals, which is
 CC responsible for the binding of MAP1B to microtubules.
 CC !- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated
 CC from MAP1B by proteolytic processing. It is free to associate with

CC both MAP1A and MAP1B. It interacts with the amino-terminal region
 CC of MAP1B (By similarity).
 CC -!- SIMILARITY: TO MAP1A.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L06237; AAA18904.1; -.
 DR Genew; HGNC:6836; MAP1B.
 DR MIM; 157129; -.
 DR GO; GO:0005875; C:microtubule associated complex; TAS.
 DR InterPro; IPR000102; MAP1B_neuraxin.
 DR Pfam; PF00414; MAP1B_neuraxin; 10.
 DR PROSITE; PS00230; MAP1B_NEURAXIN; 6.
 KW Microtubules; Repeat; Phosphorylation.
 FT CHAIN ? 2468 MAP1 LIGHT CHAIN LC1.
 FT REPEAT 1878 1894 MAP1B 1.
 FT REPEAT 1895 1911 MAP1B 2.
 FT REPEAT 1912 1928 MAP1B 3.
 FT REPEAT 1929 1945 MAP1B 4.
 FT REPEAT 1946 1962 MAP1B 5.
 FT REPEAT 1963 1979 MAP1B 6.
 FT REPEAT 1997 2013 MAP1B 7.
 FT REPEAT 2014 2030 MAP1B 8.
 FT REPEAT 2031 2047 MAP1B 9.
 FT REPEAT 2048 2064 MAP1B 10.
 FT DOMAIN 589 790 LYS-RICH (HIGHLY BASIC, CONTAINS MANY
 FT KKEE AND KKEI/V REPEATS).
 SQ SEQUENCE 2468 AA; 270618 MW; 540839CBDF09D461 CRC64;

Query Match 4.9%; Score 288; DB 1; Length 2468;
 Best Local Similarity 20.2%; Pred. No. 0.0015;
 Matches 251; Conservative 166; Mismatches 441; Indels 386; Gaps 56;

Qy 13 STDSPPR--PPPAFKYQFVTEPEDEEDEEEE-----EED-----EEEDDED 50
 :|| |: | : :||:::|:| :|| || |
 Db 625 ATDVKPKAAKEKTVKKETKVKPEDKKEEKEKPKKEVAKKEDKTPIKKEEKPKKEEVKKEV 684
 Qy 51 LEELEVLERKPAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWER 110
 :|:: |:| | : : : : : : :|:
 Db 685 KKEIKKEEKK-----EPKKEVKKETPPKEVKKEVKKEEKKEVKKE---EK 726
 Qy 111 SPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAPSTPAAPKRRG-- 168
 | || | : | | : | | | : | || :|
 Db 727 EPKKEIKKLPKDAKKSSTPLSEAKKPAALKPKVPKKEESVKKDSVA---AGKPKEKGKI 782
 Qy 169 -----SGSVDETLFAL-----PA-----ASEPVI PSSAEKIMDLME 199
 | | : | || | : : | : | |
 Db 783 KVIKKEGKAAEA VAAAVGTGATTAAVMAAAGIAAIGPAKELEAERSLMSSPEDLTDFEE 842
 Qy 200 QPGNTVSSGQEDFPSV-LLETAASLPSLSPLSTVSFKEHGYLGNL SAVSSSEGTIEETLN 258
 | : : | : | : | : : : | | || | |

Db	843	LKAEVDVTKDIPQLELIEDEEKLKETEPVEAYVIQKEREVTKGPAESPDEG-ITTEG	901
Qy	259	EASKELPERATNPVFNRDLAEFSELEYSEMSSFKGSPKGESAILVENTK-EEVIVRSKD	317
Db	902	EGECEQTPEELEPVEKQGVDDIEKFE--DEGAGFEES--SETGDYEEKAETEEAEPEED	957
Qy	318	KEDLVC-SAALHSP-----QESPVGKEDRVVSPEKTMDFNEMQMSV	358
Db	958	GEEHVCVSASKHSPTEDDEESAKAEADAYIREKRESVASGDDRA---EEDMD---EAIEKG	1011
Qy	359	VAPVREEYADFKPFEQAWEVK-DTYEGSRDVLAAARANVESKVDRKCLEDLSLEQ-----	410
Db	1012	EAEQSEEEADEE--DKAEDAREEEYEPEK--MEAEDYVMAVVDKAAEAGGAEEQYGLTT	1067
Qy	411	--KSLGKDSEGR-----NEDASFPSTPEPVKDSSRAYITCASFTSATESTT	454
Db	1068	PTKQLGAQSPGREPASSIHDETLPGGSESEATASDEENREDQPEEFTATSGYTQSTIEIS	1127
Qy	455	ANTFPL-----LEDHTSENKTDEK-----KIEERKAQIITEKTS-PKTSNPFLVAV	499
Db	1128	SEPTPMDEMSTPRDVMSETNNEETESPSQEFVNITKYESSLYSQEYSKPADVTPLNGFS	1187
Qy	500	QDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDL---	556
Db	1188	EGSKTD--ATDGKDYNASASTISPPSSMEED---KFSRSALRDAYCSEVKASTTLDIKDS	1242
Qy	557	--VQTSEAIQESLYPTAQLCP-----SFE-----EAEATPSVLPDIV	592
Db	1243	ISAVSSEKVSPSKSPSLSPSPSPLEKTPLGERSVNFSLTPNEIKVSAEAEVAPVSPEVT	1302
Qy	593	ME-----APLNSLLPSAG-----ASVVQ-----	610
Db	1303	QEVVEEHCASPEDKTLEVVSPSQSVTGSAGHTPPYQSPTEKSSHLPTIEVKPPAVPVS	1362
Qy	611	-----PSVSPLEAPPVSYDSIK--LEPENPPP-----YEEAMNVALKALG	649
Db	1363	FEFSDAKDENERASVSPMDEPVPDSESPIEKVLSPLRSPPLIGSESAYESFLSADDKASG	1422
Qy	650	TKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPD-FSNYSEIA-----KF	701
Db	1423	-----RGAESPF-----EEKSGKQGSPPQVSPVSEMTSTSLYQDKQ	1458
Qy	702	EKSVPHEAELVEDSSPE-----SEPVDLFSDDSIPEVPQTQ-----EEAV	741
Db	1459	EGKSTDFAPIKEDFGQEKKTDDVEAMSSQPALALDERKLGDVSPQTQIDVSQFGSFKEDTK	1518
Qy	742	MLMKE-----SLTEVSETVAQ----HKEERLSASPQELG-----KPYLESFQPNLHSTK	786
Db	1519	MSISEGTVSDKSATPVDEGVAEDTYSHMEGVASVSTASVATSSFPEPTTDDVSPSLH---	1575
Qy	787	DAASNDIPTLTK-KEKISLQMEEFNIAISNDDLSSKEDKIKESETFSDSSPIEIIDEF	845
Db	1576	--AEVGSPHSTEVDDSLSVSVVQTPTT-FQETEMSPSKEECPR-----	1615
Qy	846	PTFVSAKDDSPKLAKEYTDLE--VSDKSEIANIQSGADSLPCLELPCDLSFKN-----	896
Db	1616	PMSISPPDFSPKTAKSRTPVQDHRSEQSSM-SIEFGQES-PEQSLAMDFSQSPDHPTVG	1673

Qy 897 -----IYPKDE-VHVSDEFSENRSSVSKASISPSNV 926
 Db 1674 AGVLHITENGPTEVDYSPSDMQDSSLSHKIPPMEEPSYTQDNDLSELISVSQVEASPSTS 1733
 Qy 927 SALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAE 970
 Db 1734 SAHTP-SQIASPLQEDTLSDVAPPR-----DMSLYASLTSE 1768

RESULT 15

MAPB_MOUSE

ID MAPB_MOUSE STANDARD; PRT; 2464 AA.
 AC P14873;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))
 DE [Contains: MAP1 light chain LC1].
 GN MAP1B OR MTAP1B OR MTAP5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND DOMAIN.
 RC STRAIN=Swiss Webster; TISSUE=Brain;
 RX MEDLINE=90094539; PubMed=2480963;
 RA Noble M., Lewis S.A., Cowan N.J.;
 RT "The microtubule binding domain of microtubule-associated protein
 RT MAP1B contains a repeated sequence motif unrelated to that of MAP2
 RT and tau.";
 RL J. Cell Biol. 109:3367-3376(1989).
 CC -!- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.
 CC PHOSPHORYLATED MAP1B MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES
 CC THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAP1B BINDS TO AT LEAST
 CC TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS
 CC MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
 CC STABILIZING MICROTUBULES.
 CC -!- SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE
 CC WITH MAP1A AND MAP1B PROTEINS.
 CC -!- DOMAIN: Has a highly basic region with many copies of the sequence
 CC KKEE and KKEI/V, repeated but not at fixed intervals, which is
 CC responsible for the binding of MAP1B to microtubules.
 CC -!- PTM: LC1 IS COEXPRESSED WITH MAP1B. IT IS A POLYPEPTIDE GENERATED
 CC FROM MAP1B BY PROTEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH
 CC BOTH MAP1A AND MAP1B. IT INTERACTS WITH THE AMINO-TERMINAL REGION
 CC OF MAP1B.
 CC -!- SIMILARITY: TO MAP1A.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

```

CC -----
DR EMBL; X51396; CAA35761.1; -.
DR PIR; S07549; QRMSPL.
DR MGD; MGI:1306778; Mtap1b.
DR GO; GO:0016358; P:dendrite morphogenesis; IMP.
DR GO; GO:0001578; P:microtubule bundling; IMP.
DR InterPro; IPR000102; MAP1B_neuraxin.
DR Pfam; PF00414; MAP1B_neuraxin; 10.
DR PROSITE; PS00230; MAP1B_NEURAXIN; 7.
KW Microtubules; Repeat; Phosphorylation.
FT CHAIN      ?      2464      MAP1 LIGHT CHAIN LC1.
FT REPEAT      1874      1890      MAP1B 1.
FT REPEAT      1891      1907      MAP1B 2.
FT REPEAT      1908      1924      MAP1B 3.
FT REPEAT      1925      1941      MAP1B 4.
FT REPEAT      1942      1958      MAP1B 5.
FT REPEAT      1959      1975      MAP1B 6.
FT REPEAT      1993      2009      MAP1B 7.
FT REPEAT      2010      2026      MAP1B 8.
FT REPEAT      2027      2043      MAP1B 9.
FT REPEAT      2044      2060      MAP1B 10.
FT DOMAIN      589      787      LYS-RICH (HIGHLY BASIC, CONTAINS MANY
FT                                     KKEE AND KKEI/V REPEATS).
SQ SEQUENCE    2464 AA;  270408 MW;  FBD3DD99CFDBDA87 CRC64;

```

```

Query Match          4.9%; Score 284; DB 1; Length 2464;
Best Local Similarity 20.7%; Pred. No. 0.0021;
Matches 233; Conservative 159; Mismatches 424; Indels 312; Gaps 51;

```

```

Qy      31 EPEDEEDEEEEEDEED-----DEDLEELE-----VLERKPAAG-----LSAAAVP 71
      | | :| |||: || : | | | :| :| |
Db    1009 EAEQSEEEGEEEDKAEDAREEGYEPDKTEAEDYVMAVADKAAEAGVTEEQYGYLGTSKQ 1068

Qy      72 PAAAPLLDFSS----DSVPPAPRGPLPAAPPAAPERQP-----SWERSPAAPA 116
      | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    1069 PGIQSPSREPASSIHDETLPGGSESEATASDEENREDQPEEFTATSGYTQSTIEISSEPT 1128

Qy     117 P---SLPPAAAVLPSKLPEDDEPPARP-----PPPPPAGASPLAEP-- 155
      | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    1129 PMDEMSTPRDVMDETNNNEETESPSQEFVNITKYESSLYSQEYSKPAVASFNGLSEGSKT 1188

Qy     156 -----APPSTPAAPKRRSGSVDETLFALPA-----ASEPVIPISSAEKIMDLMEQ 200
      | || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    1189 DATDGKDYNASASTISPP-----SSMEEDKFSKSALRDAYCSEEKELKASAE--LDIKDV 1241

Qy     201 PGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLGNL SAVSSSEG TIEETLNEA 260
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    1242 SDERLS-----PAKSPSLSP-----SPPSPIEKT----- 1265

Qy     261 SKELPERATNPVFNRLAEFS----ELEYSEMSSFGSGPKGESAILVEN--TKEEVIVR 314
      | ||: | || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    1266 --PLGERSVN-----FSLTPNEIKVSAEGEARSVSPGVTQAVVEEH CASPEEKTLE 1314

Qy     315 SKDKEDLVCSAALHSP-QESPVGKEDRVVSPEKTMDFNEMQMSVVA-PVREEYADFK-- 370
      | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    1315 VVSPSQSVTGSAGHTPYQSP-----TDEKSSHLPTVSENAQAVPVSF EFSEAKDE 1366

```

Qy 371 -----PFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLED--SLEQKSLGKDS----- 417
| : : | : | : : | : | : | : | :
Db 1367 NERASLSPMDE--PVPDSESPVEKVLSPLRSPPLLGSSESPYEDFLSADSKVLGRRSESPF 1424

Qy 418 EGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPILLEDHTSENKT----- 470
| : : | : | : | : : : : : : : : : : : :
Db 1425 EGKNGKQGFDPDRESPVSDLT----STGLYQDKQEEKSTGFIPIKEDFGPEKKTSDVETMS 1480

Qy 471 -----DEKKI-----EERKAQIITEKTSPKTSNPFLVAVQDSEAD 505
| : : | : | : | : : | : : | : :
Db 1481 SQSALALDERKLGGDVSPTQIDVSQFGSFKEDTKMSISEGTVSDKSATPVDEGV--AEDT 1538

Qy 506 YVTTDTLSKVTEAAV--SNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAI 563
| : : : | : | : | : | : : : : : : : : : : : :
Db 1539 YSHMEGVASVSTASVATSSFPPTDD--VSPSLHAEVGSHPHSTEVDDSLSVSVVQTPTTF 1597

Qy 564 QES-LYPTAQLCP---SFEEAEATP-----SPVLDPDIMEAPLNSLL-- 601
| : : | : : | : : : : : : : : : : : : : : : :
Db 1598 QETEMSPSKEECPRPMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSFAMD 1657

Qy 602 -----PSAGASVVQPSVSPLAAPPVSYD-----SIKLEPENPPPYEEAMNVA 644
| : | | | : : : | : | | : : | : | : : : : :
Db 1658 FSRQSPDHPTLGASVLHITEN---GPTEVDYSPCDIQDSSLSHKIPPTTEPSYTDNDLS 1714

Qy 645 LKALGTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDFSNYSEIAKFEKS 704
: : : | : : | : | : : | : | : : | : : : :
Db 1715 -ELISVSQVEASPSTSSAHTPS-----QIASPLQEDTLSDVVPREMSLYASLA----- 1762

Qy 705 VPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVML---MKESLTEVSETVAQHKE 760
: | : | : | : | : | : | : | : : : : | : | : | :
Db 1763 ---SEKVQ--SLEGEKLSPKSDIS---PLTPRESSPLYSPGFSDDSTSAAKETAAAH-- 1810

Qy 761 ERLSASP---QELGKPY-----LESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFN 810
: | : | : | : : : : : : : : : : : : : : : :
Db 1811 -QASSPPIDAATAEPYGFRRSMLFDTMQHHLALNRDLTTSSV---EKDSGGKTPGDFN 1865

Qy 811 TAIYSNDDLLSSKEDIKESETFSDSSPIEIDEFPTFVSAKDDSPK---LAKEYTDLE 866
| : : | : : : | : | : | : : : : | : : | : :
Db 1866 YAYQKPENAAAGSPDEEDYDYE--SQEKTIRTHDVVRYYYEKTERTIKSPCDSGYSYETIE 1923

Qy 867 VSDKSEIANIQSGADSLPCLLELPCLDSFKNIYPKDEVHVSDEFSENRSSVSKAS----- 920
: | : : | : : : | : : | : | : : : : : : :
Db 1924 KTTKTP---EDGG-----YTCEITEKTTTRTPEEGGYSEISEKTTTRTPEVSGYTYEK 1972

Qy 921 -----ISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRS 962
: : : : : | : : | : : | : : | : : | : :
Db 1973 TERSRRLDDISNGYDDTEDGGHTLGDCSYSYETTEKITSFPESESYS 2020

Search completed: December 19, 2003, 15:35:43
Job time : 23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2003, 15:32:53 ; Search time 46 Seconds
(without alignments)
6524.243 Million cell updates/sec

Title: US-09-830-972-2
Perfect score: 5848
Sequence: 1 MEDIDQSSLVSSSTDSPRP.....VKDAMAKIQAKIPGLKRKAD 1163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description

1	5312.5	90.8	1162	11	Q8BGM9	Q8bgm9 mus musculu
2	5307	90.7	1163	11	Q8K3G8	Q8k3g8 mus musculu
3	4501.5	77.0	1046	11	Q8BGK7	Q8bgk7 mus musculu
4	3627.5	62.0	986	4	Q8IUA4	Q8iua4 homo sapien
5	2926	50.0	639	11	Q8K290	Q8k290 mus musculu
6	1416	24.2	375	11	Q8BHF5	Q8bhf5 mus musculu
7	1314.5	22.5	356	11	Q8BH78	Q8bh78 mus musculu
8	1304	22.3	357	11	Q8K3G7	Q8k3g7 mus musculu
9	1283.5	21.9	392	4	Q96B16	Q96b16 homo sapien
10	844	14.4	179	6	Q9GM33	Q9gm33 macaca fasc
11	792	13.5	780	11	Q8K4S4	Q8k4s4 mus musculu
12	788	13.5	780	11	Q8K0T0	Q8k0t0 mus musculu
13	762.5	13.0	760	13	Q90638	Q90638 gallus gall
14	700	12.0	643	11	Q8CCU2	Q8ccu2 mus musculu
15	685	11.7	199	4	Q9BQ59	Q9bq59 homo sapien
16	671	11.5	267	11	Q63765	Q63765 rattus sp.
17	669	11.4	208	13	Q90637	Q90637 gallus gall
18	625.5	10.7	236	11	Q8VBU0	Q8vbu0 rattus norv
19	625.5	10.7	237	11	Q8C6D5	Q8c6d5 mus musculu
20	586	10.0	595	5	Q9VMV9	Q9vmv9 drosophila
21	532	9.1	224	5	Q9VMW1	Q9vmw1 drosophila
22	520	8.9	202	5	Q9VMW2	Q9vmw2 drosophila
23	520	8.9	222	5	Q9VMW4	Q9vmw4 drosophila
24	520	8.9	234	5	Q9VMW3	Q9vmw3 drosophila
25	517	8.8	2484	5	Q9U347	Q9u347 caenorhabdi
26	503.5	8.6	2607	5	Q23187	Q23187 caenorhabdi
27	377	6.4	2768	5	Q9VC00	Q9vc00 drosophila
28	347.5	5.9	10578	5	Q8ISF5	Q8isf5 caenorhabdi
29	343.5	5.9	18519	5	Q8ISF6	Q8isf6 caenorhabdi
30	343.5	5.9	18534	5	Q8ISF7	Q8isf7 caenorhabdi
31	335	5.7	5412	5	Q9W596	Q9w596 drosophila
32	331	5.7	4900	5	Q9N541	Q9n541 caenorhabdi
33	328.5	5.6	5327	5	O76891	O76891 drosophila
34	322	5.5	7962	4	Q10465	Q10465 homo sapien
35	320	5.5	222	5	Q23188	Q23188 caenorhabdi
36	317.5	5.4	17352	5	Q95YM2	Q95ym2 procambarus
37	313.5	5.4	1444	5	Q9VTN2	Q9vtn2 drosophila
38	313.5	5.4	1514	5	Q8SY55	Q8sy55 drosophila
39	309.5	5.3	1852	3	Q9C2H4	Q9c2h4 neurospora
40	308	5.3	2362	5	Q9VYD1	Q9vyd1 drosophila
41	307	5.2	34350	4	Q8WZ42	Q8wz42 homo sapien
42	306	5.2	842	5	Q9VGC9	Q9vgc9 drosophila
43	306	5.2	864	5	Q9VGC8	Q9vgc8 drosophila
44	305.5	5.2	9196	5	Q8IQ87	Q8iq87 drosophila
45	304	5.2	864	5	Q95U45	Q95u45 drosophila

ALIGNMENTS

RESULT 1

Q8BGM9

ID Q8BGM9 PRELIMINARY; PRT; 1162 AA.

AC Q8BGM9;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Db	297	AMLVENTKEEVIVRSKDKEDLVCSAALHNPQESPATLTKVVKEDGVMSPEKTMDIFNEMK	356
Qy	356	MSVVAPVREEYADFKPFQAWVEVKDITYEGSRDVLAAARANVESKVDRKCLEDSEQKSLGK	415
Db	357	MSVVAPVREEYADFKPFQAWVEVKDITYEGSRDVLAAARANMESKVDKKCFEDSLEQKGHGK	416
Qy	416	DSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKI	475
Db	417	DSESRNENASFPRTPELVKDGSRAYITCDSFSSATESTANIFPVLEDHTSENKTDEKKI	476
Qy	476	EERKAQIIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEA	535
Db	477	EERKAQIIITEKTSPKTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA	536
Qy	536	CESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEA	595
Db	537	CESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEA	596
Qy	596	PLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIK	655
Db	597	PLNSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIK	656
Qy	656	EPESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDS	715
Db	657	EPESFNAAAQEAEPYISIIACDLIKETKLSTEPSPEFSNYSEIAKFEKSVDPHCELVDDS	716
Qy	716	SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHK-EERLSASPQELGKPY	774
Db	717	SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVTQHKHKERLSASPQEVGKPY	776
Qy	775	LESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNNTAIYSNDDLSSKEDKIKESETFS	834
Db	777	LESFQPNLHITKDAASNEIPTLTKEKISLQMEEFNNTAIYSNDDLSSKEDKMKESSETFS	836
Qy	835	DSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSF	894
Db	837	DSSPIEIIDEFPTFVSAKDDSP---KEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSF	893
Qy	895	KNIYPKDEVHVSDEFSENRRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPS	954
Db	894	KNTYPKDEAHVSDEFKSRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEKKLPS	953
Qy	955	DTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYI	1014
Db	954	DTEKEDRSLTAVLSAELNKTTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYI	1013
Qy	1015	ALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTI	1074
Db	1014	ALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTI	1073
Qy	1075	KELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQID	1134
Db	1074	KELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQID	1133
Qy	1135	HYLGLANKSVKDAMAKIQAKIPGLKRKAD	1163

Qy	356	MSVVAPVREEYADFKPFQAWVEKDTYEGSRDVLAAARANVESKVDKCLSDLEQKSLGK	415
Db	357	MSVVAPVREEYADFKPFQAWVEKDTYEGSRDVLAAARANMESKVDKCKCFEDSLEQKSHGK	416
Qy	416	DSEGRNEDASFPSTPEPVKDSRRAYITCASFTSATESTANTFPILLEDHTSENKTDEKKI	475
Db	417	DSESRNENASFPSTPELVKDGSRAYITCDSFTSATESTAANIFPVLEDHTSENKTDEKKI	476
Qy	476	EERKAQIIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEA	535
Db	477	EERKAQIIITEKTSPKTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA	536
Qy	536	CESELNEATGTKIAYETKVLDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEA	595
Db	537	CESELNEATGTKIAYETKVLDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEA	596
Qy	596	PLNSLLPSAGASVVPSPLEAPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIIK	655
Db	597	PLNSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPPPYEEAMSVALKTSDAKEEIIK	656
Qy	656	EPESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPHEAELVEDS	715
Db	657	EPESFNAAAQEAAPYISIIACDLIKETKLSTEPSPGFSNYSEIAKFEKSVPDHCELVDSDS	716
Qy	716	SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHK-EERLSASPOELGKPY	774
Db	717	SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVTQHKHKERLSASPOEVGKPY	776
Qy	775	LESFQPNLHSTKDAASNDIPTLTKKKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFS	834
Db	777	LESFQPNLHITKDAASNEIPTLTKKKETISLQMEEFNTAIYSNDDLSSKEDKMKESSETFS	836
Qy	835	DSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSF	894
Db	837	DSSPIEIIDEFPTFVSAKDDSP--KEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSF	893
Qy	895	KNIYPKDEVHVSDEFSENSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPS	954
Db	894	KNTYPKDEAHVSDEFKSRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEKKLPS	953
Qy	955	DTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAY	1013
Db	954	DTEKEDRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAY	1013
Qy	1014	IALALLSVTISFRIYKGVIIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNST	1073
Db	1014	IALALLSVTISFRIYKGVIIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNST	1073
Qy	1074	IKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLIILALISLFSIPVIYERHQVQI	1133
Db	1074	IKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLIILALISLFSIPVIYERHQAQI	1133
Qy	1134	DHYLGLANKSVKDAMAKIQAKIPGLKRKAD	1163
Db	1134	DHYLGLANKSVKDAMAKIQAKIPGLKRKAE	1163

Q8BGK7

Query Match 77.0%; Score 4501.5; DB 11; Length 1046;
Best Local Similarity 86.9%; Pred. No. 5.5e-221;
Matches 910; Conservative 40; Mismatches 68; Indels 29; Gaps 4.

[illegible]

Db 183 LVENTKEEVIIVRSKDKEDLVCSAALHNPQESPATLTKVVKEDGVMSPEKTMDFNEMKMS 242

Qy 358 VVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLEDSEQKSLGKDS 417
 |||:|||||:|||||

Db 243 VVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANMESKVDKKCFEDSLEQKGHGKDS 302

Qy 418 EGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPILLEDHTSENKTDEKKIEE 477
 |||:|||||:|||||

Db 303 ESRNENASFPRTPELVKDGSRAYITCDSFSSATESTAANIFPVLEDHTSENKTDEKKIEE 362

Qy 478 RKAQIIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACE 537
 |||:|||||:|||||

Db 363 RKAQIIITEKTSPKTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEACE 422

Qy 538 SELNEATGTKIAYETKVLDVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPL 597
 |||:|||||:|||||

Db 423 SELNEATGTKIAYETKVLDVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEAPL 482

Qy 598 NSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEP 657
 |||:|||||:|||||

Db 483 NSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIKEP 542

Qy 658 ESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSP 717
 |||:|||||:|||||

Db 543 ESFNAAAQAEAPYISIIACDLIKETKLSTEPSPEFSNYSEIAKFEKSVDPHCELVDSSP 602

Qy 718 ESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHK-EERLSASPQELGKPYLE 776
 |||:|||||:|||||

Db 603 ESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVTQHKHKERLSASPQEVGKPYLE 662

Qy 777 SFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDS 836
 |||:|||||:|||||

Db 663 SFQPNLHITKDAASNEIPTLTKETISLQMEEFNTAIYSNDDLSSKEDKMKESSETFSDS 722

Qy 837 SPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKN 896
 |||:|||||:|||||

Db 723 SPIEIIDEFPTFVSAKDDSP---KEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKN 779

Qy 897 IYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDT 956
 |||:|||||:|||||

Db 780 TYPKDEAHVSDEFKSRSSSVKPLLLPNVSALESQIEMGNIVKPKVLTKEAEKKLPSDT 839

Qy 957 EKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIAL 1016
 |||:|||||:|||||

Db 840 EKEDRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIAL 899

Qy 1017 ALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKE 1076
 |||:|||||:|||||

Db 900 ALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKE 959

Qy 1077 LRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHY 1136
 |||:|||||:|||||

Db 960 LRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHY 1019

Qy 1137 LGLANKSVKDAMAKIQAKIPGLKRKAD 1163
 |||:|||||

Db 1020 LGLANKSVKDAMAKIQAKIPGLKRKAE 1046

RESULT 4

Q8IUA4

ID Q8IUA4 PRELIMINARY; PRT; 986 AA.
 AC Q8IUA4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE RNT4 (RTN4).
 GN RTN4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22376540; PubMed=12488097;
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL J. Mol. Biol. 325:299-323(2003).
 DR EMBL; AY102285; AAM64244.1; -.
 DR EMBL; AY123245; AAM64249.1; -.
 DR EMBL; AY123246; AAM64250.1; -.
 DR EMBL; AY123247; AAM64251.1; -.
 DR EMBL; AY123248; AAM64252.1; -.
 DR EMBL; AY123249; AAM64253.1; -.
 DR EMBL; AY123250; AAM64254.1; -.
 SQ SEQUENCE 986 AA; 108449 MW; 0CDE8F647036415A CRC64;

Query Match 62.0%; Score 3627.5; DB 4; Length 986;
 Best Local Similarity 75.4%; Pred. No. 1.6e-176;
 Matches 745; Conservative 96; Mismatches 126; Indels 21; Gaps 13;

Qy 195 MDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSVFKEHGYLGNL SAVSSSEGTIE 254
 ||| |||||:|:||||||||||||||||||||||| |||| ||||| | :|||:
 Db 1 MDLKEQPGNTISAGQEDFPSVLLETAASLPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQ 60
 Qy 255 ETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSFSGKSPKGESAILVENTKEEVIVR 314
 | :||| |||: | :||| ||||| ||||| ||| |||:| | :|||:
 Db 61 ENVSEASKEVSEKAKTLLIDRLTEFSELEYSEMGSFVSPKAESAVIVANPREEIIVK 120

Qy	315	SKDKED-LVCSAALHSPQESPVG-----KEDRVVSPEKTMDFINEMQMSVVAPVREEYAD	368
Db	121	NKDEEEKLVSNNILHNQQELPTALTCLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYAD	180
Qy	369	FKPFEQAWEVKDTYEGSRDLAA----RANVESKVDRKCLEDSLEQKSLGKDSEGRNEDA	424
Db	181	FKPFERVWEVKDSKEDS-DMLAAGGKIESNLESKVDDKCFADSLEQTNHEKDSSESSNDDT	239
Qy	425	SFPSTPEPVKDSSRAYITCASFT-SATESTTANTFPLLEDHTSENKTDEKKIEERKAQII	483
Db	240	SFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLGDPTSENKTDEKKIEEKKAQIV	299
Qy	484	TEK-TSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNE	542
Db	300	TEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNE	359
Qy	543	ATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSVLPDIMEAPLNSLLP	602
Db	360	VTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSVLPDIMEAPLNSAVP	419
Qy	603	SAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKAL-GTKEGIKEPESFN	661
Db	420	SAGASVIQPSSSPLEA-SSVNYESIKHEPENPPPYEAMSVSLKKVSGIKEEIKEPENIN	478
Qy	662	AAVQETEAPYIISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESEP	721
Db	479	AALQETEAPYIISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEP	538
Qy	722	VDLFSDDSIPEVPQTQEEAVMLMKESLTEVS-ETVAQHK-EERLSASPQELGKPYLESFQ	779
Db	539	VDLFSDDSIPDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFK	598
Qy	780	PNLHSTKDA-ASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSP	838
Db	599	LSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI SKEAQIRETETFSDDSP	658
Qy	839	IEIIDEFPFVSAKDDS-PKLAKEYTDLEVSDKSEIANIQSGADSLPCLLELPCDLSFKNI	897
Db	659	IEIIDEFPPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKN	718
Qy	898	YPK--DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLP	955
Db	719	QPKVEEKISFSDDFSNGSATS KVVLLLPDVSALATQAEIESIVKPKVLVKEAEKKLP	778
Qy	956	TEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIA	1015
Db	779	TEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIA	838
Qy	1016	LALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIK	1075
Db	839	LALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIK	898
Qy	1076	ELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDH	1135
Db	899	ELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHOAQIDH	958

Qy 1136 YLGLANKSVKDAMAKIQAKIPGLKRRKAD 1163
|||||:|||||:|||||:|||||:|||||:
Db 959 YLGLANKNVKDAMAKIQAKIPGLKRRKAE 986

RESULT 5

Q8K290

ID Q8K290 PRELIMINARY; PRT; 639 AA.
AC Q8K290;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN RTN4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC032192; AAH32192.1; -.
DR MGD; MGI:1915835; Rtn4.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
KW Hypothetical protein.
SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

Query Match 50.0%; Score 2926; DB 11; Length 639;
Best Local Similarity 91.6%; Pred. No. 4.7e-141;
Matches 588; Conservative 20; Mismatches 30; Indels 4; Gaps 2;

Qy 523 MPEGLTPLDVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAE 582
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MPEGLTPLDVQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAE 60

Qy 583 TPSPVLPDIVMEAPLNSLLPSAGASVVQSPVSPLEAPPVSYDSIKLEPENPPPYEEAMN 642
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 TPSPVLPDIVMEAPLNSLLPSTGASVAQSPASPLEVPSPVSYDGIKLEPENPPPYEEAMS 120

Qy 643 VALKALGTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDFSNYSEIAKFE 702
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 VALKTSDAKEEIKEPESFNAAAQAEAPYISACDLIKETKLSTEPSPEFSNYSEIAKFE 180

Qy 703 KSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHK-EE 761
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 KSVPDHCELVDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVTQHKHKE 240

Qy 762 RLSASPQELGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLLS 821
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 RLSASPQEVGKPYLESFQPNLHITKDAASNEIPTLTKEKISLQMEEFNTAIYSNDDLLS 300

Qy 822 SKEDKIKESETFSDSSPIEIIDFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGAD 881
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 SKEDKMKESETFSDSSPIEIIDFPTFVSAKDDSP--KEYTDLEVSNKSEIANVQSGAN 357


```

Db      188 ----- 187
Qy      781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE 840
Db      188 ----- 187
Qy      841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900
Db      188 ----- 187
Qy      901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED 960
Db      188 ----- 187
Qy      961 RLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 1020
          |||||||||||||||||||||||||||||||||||||||
Db      188 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 232
Qy      1021 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080
          |||||||||||||||||||||||||||||||||||||||
Db      233 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 292
Qy      1081 FLVDDLVDLKLFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 1140
          |||||||||||||||||||||||||||||||||||||||
Db      293 FLVDDLVDLKLFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 352
Qy      1141 NKSVDAMAKIQAKIPGLKRKAD 1163
          |||||||||||||||||||:
Db      353 NKSVDAMAKIQAKIPGLKRKAE 375

```

RESULT 7

Q8BH78

```

ID   Q8BH78      PRELIMINARY;      PRT;      356 AA.
AC   Q8BH78;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   RTN4.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

```


Qy 601 LPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF 660
 Db 169 ----- 168
 Qy 661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720
 Db 169 ----- 168
 Qy 721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP 780
 Db 169 ----- 168
 Qy 781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE 840
 Db 169 ----- 168
 Qy 841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900
 Db 169 ----- 168
 Qy 901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED 960
 Db 169 ----- 168
 Qy 961 RLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 1020
 Db 169 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 213
 Qy 1021 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080
 Db 214 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 273
 Qy 1081 FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 1140
 Db 274 FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLA 333
 Qy 1141 NKSVKDAMAKIQAKIPGLKRKAD 1163
 Db 334 NKSVKDAMAKIQAKIPGLKRKAE 356

RESULT 8

Q8K3G7

ID Q8K3G7 PRELIMINARY; PRT; 357 AA.
 AC Q8K3G7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Nogo-B.
 GN RTN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

Db	169	-----	168
Qy	661	NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Db	169	-----	168
Qy	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Db	169	-----	168
Qy	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Db	169	-----	168
Qy	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Db	169	-----	168
Qy	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED	960
Db	169	-----	168
Qy	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALL	1019
Db	169	-----VVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALL	213
Qy	1020	SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR	1079
Db	214	SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR	273
Qy	1080	LFLVDDLVDLKFVAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGL	1139
Db	274	LFLVDDLVDLKFVAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGL	333
Qy	1140	ANKSVKDAMAKIQAKIPGLKRKAD	1163
Db	334	ANKSVKDAMAKIQAKIPGLKRKAE	357

RESULT 9

Q96B16

ID Q96B16 PRELIMINARY; PRT; 392 AA.
AC Q96B16;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (RTN4).
GN RTN4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

```

RN      [2]
RP      SEQUENCE FROM N.A.
RA      Oertle T., van der Putten H., Schwab M.E.;
RT      "Genomic Structure and Functional Characterization of the Promoter
RT      Structures of Human and Mouse Nogo/Rtn-4.";
RL      Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

```

Query Match 21.9%; Score 1283.5; DB 4; Length 392;
Best Local Similarity 29.4%; Pred. No. 1.1e-57;
Matches 346; Conservative 11; Mismatches 20; Indels 801; Gaps 7;

Qy	346	KTMDIFNEMQMSVVAPVREEYADFKPFQAWQVVDYEGSRDVLAAARANVESKVDRKCLE	405
Db	205	-----	204
Qy	406	DSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHT	465
Db	205	-----	204
Qy	466	SENKTDEKKIEERKAQIIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPE	525
Db	205	-----	204
Qy	526	GLTPDLVQEACESELNEATGTKIAYETKVLDLVQTSEAIQESLYPTAQLCPSFEEAEATPS	585
Db	205	-----	204
Qy	586	PVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVAL	645
Db	205	-----	204
Qy	646	KALGTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSV	705
Db	205	-----	204
Qy	706	PEHAELVEDSSPESEPVDFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSA	765
Db	205	-----	204
Qy	766	SPQELGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKED	825
Db	205	-----	204
Qy	826	KIKESETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPC	885
Db	205	-----	204
Qy	886	LLEPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIKSKSLT	945
Db	205	-----	204
Qy	946	KEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	1005
Db	205	-----VVDLLYWRDIKKTGVVFGASLFLLLSLTVF	234
Qy	1006	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1065
Db	235	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	294
Qy	1066	ALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI	1125
Db	295	ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI	354
Qy	1126	YERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD	1163
Db	355	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	392

RESULT 10

Q9GM33

ID Q9GM33 PRELIMINARY; PRT; 179 AA.
AC Q9GM33;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 19.9 kDa protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB049853; BAB16739.1; -.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
KW Hypothetical protein.
SQ SEQUENCE 179 AA; 19949 MW; 5F8CD4383FEE9E02 CRC64;

Query Match 14.4%; Score 844; DB 6; Length 179;
Best Local Similarity 95.5%; Pred. No. 8.5e-36;
Matches 171; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 985 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAIQKSDEGHFP 1044
:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYRGVQAIQKSDEGHFP 60
Qy 1045 RAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGA 1104
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLRFVLMWVFTYVGA 120
Qy 1105 LFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRRKAD 1163
|||||||||||||||||:|||||||:|||||||||:|||||||||:|||||||
Db 121 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 179

RESULT 11

Q8K4S4

ID Q8K4S4 PRELIMINARY; PRT; 780 AA.
AC Q8K4S4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Reticulon 1A.
GN RTN1 OR RTN-1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;
 RA Hirata T., Nomura T., Takagi Y., Sato Y., Tomioka N., Fujisawa H.,
 RA Osumi N.;
 RT "Mosaic development of the olfactory cortex with Pax6-dependent and
 RT -independent components.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB074899; BAB96551.1; -.
 DR MGD; MGI:1933947; Rtn1.
 DR InterPro; IPR001951; Histone_H4.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS00047; HISTONE_H4; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 780 AA; 83504 MW; 545F5638C576A069 CRC64;

Query Match 13.5%; Score 792; DB 11; Length 780;
 Best Local Similarity 32.5%; Pred. No. 3e-32;
 Matches 242; Conservative 105; Mismatches 260; Indels 138; Gaps 27;

Qy	517	EA AVSNMPEGLTPDLVQEACESELNEATG-----TKIAYETKVDLVQTSEAIQ-ESLY	568
		: : : : : : : : : :	
Db	76	ETASTGM--AAVPDALDHSPSSTLKDGEGACYTSLISDVCYPPRED SAYFTGILQKENGH	133
Qy	569	PTAQLCPSEFEAEATPSPVLPDIVMEAP---LNS-----LLPSAGASVVQPSVSPLEAPP	620
		: : : : : :	
Db	134	ITTSESP--EEPE--TPGPSLPEVPGMEPQGLLSSDSGIEMTPAESTEVNKILADPLDQMK	190
Qy	621	PVSYSYIKLE-----PENPPPYEEAMNVALKALGTK----EGIKEPESFNAAV----	664
		: : : : : : :	
Db	191	AEAYKYIDITRPQEAKGQEEQHPGLEDKDLDFKDKGTEVSTKAEGVRAPNQ-PAPVEGKL	249
Qy	665	-----QETEAPYISIACDLIKETKLSTEPSPDFSNYSEI-----AKFEKSVPEHAELV	712
		: : : : : : : : :	
Db	250	IKDHLFEESTFAPYIDELSD--EQHRVSLVTAPVKITLTEIEPPLMTATQETIPEKQDLC	307
Qy	713	EDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHK-----EERLSASP	767
		: : : : : : :	
Db	308	LKPSPDTVPTVTVSE-----PEDDSPGSVTPSSGTEPSAAESQKGKSVSEDELIAAIK	361
Qy	768	QELGKPYLESFQPN-----LHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSS	822
		: : : : : :	
Db	362	EAKGLSYETTESPRPVGQVADKPKTKTRSGGLPTIPS-----PLDQEASS	405
Qy	823	KEDKIKESETFSDSSPIEIIDEFPT-----FVSAKDDSPKLAK-EYTDLEVSDKSEIAN	875
		: : : : : :	
Db	406	AESGDSEIELVSE-DPMASEDALPSGYVSFGHVSGPPSPASPASIQYSILREEREAE--	462
Qy	876	IQSGADSLPCLELPCDL-SFKNIYPKDEVH-----VSDEFSENRSSVSKASISPSNVS	927
		: : : :	
Db	463	-----DSELIIE-SCDASSASEESPKREQDSPPMKPGALDAIREETGSRATEERAPSHQG	516
Qy	928	ALEPQTEMGSIVKSKSLTKEAEKKL-----PSDTEKEDRSLSAVLSAE-----	970
		: : : : : : :	

Db	517	PVEPD-PMLSFAAAALQSRPEPSSGDGASVPEPPRSQQQKPEEEAVSSSSQSPTATEIPG	575
Qy	971	-----LSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALAL	1018
		: : : : : : :	
Db	576	PLGSGLMPPLPFFNKQKAIDLLEYWRDIKQTGIVFGSFLLLLSLTQFSVSVVAYLALAA	635
Qy	1019	LSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELR	1078
		: : : : : : : : : :	
Db	636	LSATISFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKYTDCLQLYVNSTLKELR	695
Qy	1079	RLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLG	1138
		: : : : : : : :	
Db	696	RLFLVQDLVDLSLKFAVLMWLLTYVGALFNGLTLLMAVSMFTLPVVVVKHQAQVDQYLG	755
Qy	1139	LANKSVKDAMAKIQAKIPGLKRRAD	1163
		: : :	
Db	756	LVRTHINTVVAKIQAKIPGAKRHAEE	780

```

RESULT 12
Q8K0T0
ID   Q8K0T0          PRELIMINARY;          PRT;   780 AA.
AC   Q8K0T0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to reticulon 1.
GN   RTN1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RA   Strausberg R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR   EMBL; BC030455; AAH30455.1; -.
DR   MGD; MGI:1933947; Rtn1.
DR   InterPro; IPR001951; Histone_H4.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS00047; HISTONE_H4; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE      780 AA;  83572 MW;  29B47A58FC2F2027 CRC64;

Query Match          13.5%;  Score 788;  DB 11;  Length 780;
Best Local Similarity 32.4%;  Pred. No. 4.9e-32;
Matches 243;  Conservative 104;  Mismatches 256;  Indels 146;  Gaps 28;

Qy      517 EAAVSNMPEGLTPDLVQEACESELNEATG-----TKIAYETKVDLVQTSEAIQ-ESLY 568
      || : | || : | || : | : : | : | : : | : :
Db      76 ETASTGM--AAVPDALDHSPSSTLKDGEACYSLSIDVCYPPREDSAYFTGILQKENGH 133

Qy      569 PTAQLCPSFEEAEATPSPVLPDIVMEAP---LNS-----LLPSAGASVVQPSVSPLEAPP 620
      | | | || | || | ||:: | | : | : | : | : | : | :
Db      134 ITTSESP--EEPE-TPGPSLPEVPGMEPOGLSSDSGIEMTPAESTEVNKILADPLDOMK 190

```


Qy 537 ESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAP 596
 | : || | : || || | : | : | :
 Db 330 ISAIKEAKG--FSFETSE--VQQSPAV-----SAEKQEQKMKPGRPAV----- 368

Qy 597 LNSLLPSAGASVVQPSVSPLEAPPVSYDS-IKLEPENPPPYEEAMNVALKALGTKEGIK 655
 || || | || : | : | || : :
 Db 369 -----PSPLDNEASSAESGDSEIELVSEDPLAAEEVLHSNYMTFSHIGG-- 412

Qy 656 EPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDS 715
 | | || : | | : | : : || : :
 Db 413 PPPS-----PASPSIQYS----ILREEREAE LDS ELIIES 443

Qy 716 SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYL 775
 | | : | || : : : : | || | |
 Db 444 CDAS-----SASEESPKREQDSPLMKPMVMDI---IKEENSSRASASDYEASK--- 488

Qy 776 ESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSD 835
 | : : | : : : : : : :
 Db 489 -----TTESRMN-----RENLADSASYLK 507

Qy 836 SSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLLEPCDLSFK 895
 || || : || : |
 Db 508 SS-----FV-----APKVSSE----- 518

Qy 896 NIYPKDEVHVSDEFSEN---RSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKL 952
 | : | | : : : : | || : : : | :
 Db 519 ---PPTSAVSTEELKERIILKKPIETVVNQSKVS-----SKDSGKRS 558

Qy 953 PSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTA 1012
 | : | | : | : : || || || : || : | | | | : || |
 Db 559 P-----LALPLLPLFNKQKAINLLYWRDIKQTGIVFGSLLLLLFSLTQFSVSVVA 609

Qy 1013 YIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNS 1072
 | : || | | || || || || : || || : || : : || : : : ||
 Db 610 YLALAGLSATISFRIYKSVLQAVQKTDEGHPFKAYLDMEMNLSQDQIQKYTDCLQLYVNS 669

Qy 1073 TIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQ 1132
 | : || || || || || || || : || || || || || : || : : || : : : ||
 Db 670 TVKELRRLFLVQDLVDLSLKFAVLMWLLTYVGALFNGLTLLIMAVVSMFTLPVVYDKYQAQ 729

Qy 1133 IDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
 || || | : : || || || || || :
 Db 730 IDQYLGLVRTHINTVVAKIQAKIPGAKRKAE 760

RESULT 14

Q8CCU2

ID Q8CCU2 PRELIMINARY; PRT; 643 AA.

AC Q8CCU2;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Reticulon 3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;


```

Db      494 ILALLSVTISFRVYKSVIQAVQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHVNKAL 553
Qy      1075 KELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQID 1134
Db      554 KLIIRLFLVEDLVDSLKLAVFMWLMITYVGAVFNGITLLILAELLVFSVPIVYEKYKTQID 613
Qy      1135 HYLGLANKSVKDAMAKIQAKIPGL-KRKAD 1163
Db      614 HYVGIARDQTKSIVEKIQAKLPGIAKKAE 643

```

RESULT 15

Q9BQ59

```

ID      Q9BQ59      PRELIMINARY;      PRT;      199 AA.
AC      Q9BQ59;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Similar to reticulon 1.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Lung;
RA      Strausberg R.;
RL      Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC003003; AAH03003.1; -.
DR      EMBL; BC000314; AAH00314.1; -.
DR      InterPro; IPR001951; Histone_H4.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS00047; HISTONE_H4; 1.
DR      PROSITE; PS50845; RETICULON; 1.
SQ      SEQUENCE      199 AA;      22642 MW;      7CFA44CC568DF6D8 CRC64;

```

```

Query Match      11.7%; Score 685; DB 4; Length 199;
Best Local Similarity 67.0%; Pred. No. 1.2e-27;
Matches 128; Conservative 32; Mismatches 31; Indels 0; Gaps 0;

```

```

Qy      973 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKQVI 1032
Db      9 KSQAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVSVVAYLALAALSATISFRIYKSVL 68
Qy      1033 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLK 1092
Db      69 QAVQKTDEGHPFKAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLK 128
Qy      1093 AVLWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQ 1152
Db      129 AVLWVLLTYVGALFNGLTLLMAVVSMTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQ 188
Qy      1153 AKIPGLKRKAD 1163
Db      189 AKIPGAKRHAE 199

```


Search completed: December 19, 2003, 15:36:42
Job time : 51 secs